

TABLE 1				Document Number 1650775		
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
19 N		1729	NM_017258		B-cell translocation gene 1, anti-proliferative	B-cell translocation gene 1, anti-proliferative
20 L,N		1729	NM_017258		B-cell translocation gene 1, anti-proliferative	B-cell translocation gene 1, anti-proliferative
43 E,P		1698	NM_022287	Glycosaminoglycan degradation	HMm:alpha-L-iduronidase	Rattus norvegicus sulfate anion transporter (sal-1) mRNA, complete cds
55 O		1535	NM_012511	Oxidative phosphorylation	ATPase, Cu++ transporting, beta polypeptide (same as Wilson disease)	ATPase, Cu++ transporting, beta polypeptide (same as Wilson disease)
64 H		1620	NM_016991		Adrenergic, alpha 1B-, receptor	Adrenergic, alpha 1B-, receptor
72 F		1420	M57263		Hsp:PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE K	Rat protein-glutamine gamma-glutamyltransferase mRNA, complete cds
90 E		1454	U20796			Rattus norvegicus nuclear receptor Rev-Erba-beta mRNA, partial cds
134 A		1346	D87839	Alanine and aspartate metabolism, Butanoate metabolism, Glutamate metabolism, Propanoate metabolism, beta-Alanine metabolism	HHs:4-aminobutyrate aminotransferase	Rattus norvegicus mRNA for beta-alanine oxoglutarate aminotransferase, complete cds
135 A		1346	D87839	Alanine and aspartate metabolism, Butanoate metabolism, Glutamate metabolism, Propanoate metabolism, beta-Alanine metabolism	HHs:4-aminobutyrate aminotransferase	Rattus norvegicus mRNA for beta-alanine oxoglutarate aminotransferase, complete cds

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355 N		1600 NM_013086			CAMP responsive element modulator CREM	CAMP responsive element modulator
356 N		1658 NM_017334			CAMP responsive element modulator RNA editing deaminase of glutamate receptors	CAMP responsive element modulator RNA editing deaminase of glutamate receptors
360 R		1728 NM_012894				Rattus norvegicus prostaglandin E receptor EP2 subtype mRNA, complete cds
372 F,M		1482 U94708			Canalicular multispecific organic anion transporter	Canalicular multispecific organic anion transporter
373 P		1578 NM_012833				Rattus norvegicus alternatively spliced signal transducer and regulator of transcription 5a2 (STAT5a2) mRNA, partial cds
384 O		1457 U25137				Rattus norvegicus brain cytosolic acyl coenzyme A thioester hydrolase mRNA, complete cds
396 M		1464 U49694			Hsp-CYTOSOLIC ACYL COENZYME A THIOESTER HYDROLASE	
397 S		1614 NM_013214			acyl-CoA hydrolase	Rattus norvegicus brain cytosolic acyl coenzyme A thioester hydrolase mRNA, complete cds, acyl-CoA hydrolase
402 N		1734 NM_022403		Tryptophan metabolism	HHs:tryptophan 2,3-dioxygenase	Rat tryptophan-2,3-dioxygenase mRNA, complete cds
466 L		1517 X81395			Hsp LIVER CARBOXYLESTERASE 3 PRECURSOR	R norvegicus mRNA for pl 5.5 esterase (ES-3)

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651 J	1607	NM_013134	Sterol biosynthesis	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	3-hydroxy-3-methylglutaryl-Coenzyme A reductase
671 B	1445	U04808			Rattus norvegicus Sprague-Dawley putative G-protein coupled receptor (GCR) mRNA, complete cds
672 O	1492	X13722		Low density lipoprotein receptor	Rat mRNA for LDL-receptor
682 P	1627	NM_017051		Superoxide dismutase 2, mitochondrial	Superoxide dismutase 2, mitochondrial
689 M,P	1465	U55765			Rattus norvegicus RASP1 mRNA, complete cds
729 O	1429	M65762			Rattus norvegicus GABA transporter GAT-2 mRNA, complete cds
761 A	41	AA817685			Rattus norvegicus mRNA for cytochrome b5
794 A,D,E,G	1472	U68168	Tryptophan metabolism	HHs:kynureninase (L-kynurenine hydrolase)	Rattus norvegicus L-kynurenine hydrolase mRNA, complete cds
809 J	1451	U17035			Rattus norvegicus interferon inducible protein 10 (IP-10) mRNA, complete cds
811 A	1342	D63704	Pantothenate and CoA biosynthesis, Pyrimidine metabolism, beta-Alanine metabolism		Rat mRNA for dihydropyrimidinase, complete cds
812 A	1342	D63704	Pantothenate and CoA biosynthesis, Pyrimidine metabolism, beta-Alanine metabolism	HHs:dihydropyrimidinase	EST, Highly similar to DPYS_RAT DIHYDROPYRIMIDINASE [R.norvegicus], Rat mRNA for dihydropyrimidinase, complete cds

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				Fructose and mannose metabolism, Glycolysis/ Gluconeogenesis, Pentose phosphate cycle		
820 E		238	AA892395		Aldolase B, fructose-biphosphate	Aldolase B, fructose-biphosphate
825 A		381	AA946108			Rattus norvegicus laminin-5 alpha 3 chain mRNA, complete cds
851 A		1721	NM_024132		fatty acid amide hydrolase	Rattus norvegicus fatty acid amide hydrolase mRNA, complete cds
906 K		1480	U83112			Rattus norvegicus INS-1 winged helix mRNA, complete cds
912 A		1467	U59184		Bcl2-associated X protein	Bcl2-associated X protein
923 A,J		1632	NM_017076		Tumor-associated glycoprotein pE4	Tumor-associated glycoprotein pE4
945 P		1349	D88666			Rattus norvegicus mRNA for PS-PLA1, complete cds
955 M		1471	U67138			Rattus norvegicus PSD-95/SAP90-associated protein-2 mRNA, complete cds
958 I,Q		1591	NM_012977		Lectin, galactose binding, soluble 9 (Galectin-9)	Lectin, galactose binding, soluble 9 (Galectin-9)
961 A		1573	NM_012796	Glutathione metabolism	Glutathione S-transferase 1 (theta)	Glutathione S-transferase 1 (theta)
1007 A		1589	NM_012942	Bile acid biosynthesis	Cytochrom P450 (cholesterol hydroxylase 7 alpha)	Cytochrom P450 (cholesterol hydroxylase 7 alpha)
1037 I		1500	X57523		Transporter 1, ABC (ATP binding cassette)	R.norvegicus mtp1 mRNA
1099 A		1678	NM_019303		Cytochrome P450, subfamily IIF, polypeptide 1	Cytochrome P450, subfamily IIF, polypeptide 1
1114 N		586	A029917			Rattus norvegicus neuron-specific enolase (NSE) mRNA, complete cds

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1126 A,J		1143	AI231007			Rattus norvegicus cca1 mRNA, complete cds
1141 E,Q		1505	X59601			Rat mRNA for plectin
1169 E,H		1008	AI177161			Rattus norvegicus NF-E2-related factor 2 mRNA, complete cds
1173 A		1661	NM_019184	Fatty acid metabolism, Tryptophan metabolism, Fatty acid metabolism,	Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase)	Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase)
1174 N		1661	NM_019184	Tryptophan metabolism, Fatty acid metabolism,	Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase)	Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase)
1175 A,E,M		1661	NM_019184	Tryptophan metabolism	Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase)	Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase)
1183 J		485	AF013144		Hsp-DUAL SPECIFICITY PROTEIN PHOSPHATASE 5	Rattus norvegicus MAP-kinase phosphatase (cpg21) mRNA, complete cds
1221 B,F,Q		1326	D11445			Rattus norvegicus mRNA for gro, complete cds
1223 E		1423	M75281			Rat cystatin S (CysS) gene, complete cds
1246 A		1569	NM_012770	Purine metabolism	Guanylate cyclase, soluble, beta 2 (GTP pyrophosphate - lyase)	Guanylate cyclase, soluble, beta 2 (GTP pyrophosphate - lyase)
1258 I		1611	NM_013185		Hemopoietic cell tyrosine kinase	Hemopoietic cell tyrosine kinase
1271 Q		1384	L07073			Rat clathrin-associated adaptor protein homolog (p47A) mRNA, complete cds
1279 F		1477	U75916			Rattus norvegicus zonula occludens 2 protein (ZO-2) mRNA, partial cds
1305 J		1636	NM_017127	Glycerolipid metabolism	choline kinase	choline kinase
1306 J		1636	NM_017127	Glycerolipid metabolism	choline kinase	Rattus norvegicus GTP-binding protein (rab 3C) mRNA, complete cds
1394 G		1461	U37099			

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1399 C.D.G	1623	NM_017006	Glutathione metabolism, Pentose phosphate cycle	Glucose-6-phosphate dehydrogenase	Glucose-6-phosphate dehydrogenase
1409 A	560	A012802			Rattus norvegicus round spermatid protein RSP29 gene, complete cds
1411 C.D	920	A0172075	Pyruvate metabolism	HLH:hydroxyacyl glutathione hydrolase	ESTs
1426 Q	1528	Z48225			R.norvegicus mRNA for protein synthesis initiation factor eIF-2B delta subunit
1430 M	1542	NM_012545	Histidine metabolism, Phenylalanine metabolism, Tryptophan metabolism, Tyrosine metabolism	Dopa decarboxylase (aromatic L-amino acid decarboxylase)	Dopa decarboxylase (aromatic L-amino acid decarboxylase)
1447 F	1651	NM_017281		proteasome (prosome, macropain) subunit, alpha type 4	proteasome (prosome, macropain) subunit, alpha type 4
1460 C.D	1439	S76054		Keratin 8	Keratin 8
1475 J	1386	L16764		Heat shock protein 70-1, S100 calcium binding protein A1	Rattus norvegicus S100A1 gene, Rattus norvegicus heat shock protein 70 (HSP70) mRNA, complete cds
1478 A	1566	NM_012744	Alanine and aspartate metabolism, Citrate cycle (TCA cycle), Pyruvate metabolism	Pyruvate carboxylase	Pyruvate carboxylase
1479 A.G.K	1566	NM_012744	Alanine and aspartate metabolism, Citrate cycle (TCA cycle), Pyruvate metabolism	Pyruvate carboxylase	Pyruvate carboxylase
1501 A.C.F.H	690	A072634			Rattus norvegicus cytochrome P-450 2C10 mRNA, partial cds

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1507	B,Q	1105	A1229235			ESTs
1510	Q	1646	NM_017224		organic cationic transporter-like 1	organic cationic transporter-like 1
1514	B	1559	NM_012678		Tropomyosin 4	Tropomyosin 4
1520	H	1659	NM_019165		interleukin 18	interleukin 18
1521	B,Q	1601	NM_013091		Tumor necrosis factor receptor	Tumor necrosis factor receptor
1529	A,G	1599	NM_013082		Ryudocan/syndecan 2	Ryudocan/syndecan 2
1531	A	1655	NM_017300	Bile acid biosynthesis, Taurine and hypotaurine metabolism	bile acid-Coenzyme A dehydrogenase: amino acid n-acyltransferase	bile acid-Coenzyme A dehydrogenase: amino acid n-acyltransferase
1538	E	493	AF039890		Leucine arylaminopeptidase 1	Rat kidney Zn-peptidase aminopeptidase N mRNA, complete cds
1542	G,H	1643	NM_017193		kynurenine aminotransferase II	kynurenine aminotransferase II
1551	K	1633	NM_017084	Glycine, serine and threonine metabolism	Glycine methyltransferase	Glycine methyltransferase
1554	I	625	A1045440		Sialophorin (gpL115, leukosianin, CD43)	Sialophorin (gpL115, leukosianin, CD43)
1561	A,M,O	1621	NM_016995		Complement component 4 binding protein, beta	Complement component 4 binding protein, beta
1562	F,G	267	AA893552			Rattus norvegicus kallistatin mRNA, complete cds
1571	I	1446	U05014			Rattus norvegicus Sprague/Dawley PHAS-I mRNA, complete cds
1572	Q	1046	A1178828			Rattus norvegicus Sprague/Dawley PHAS-I mRNA, complete cds
1579	R	1512	X73411			Rat small nuclear ribonucleoparticle-associated protein (snRNP) mRNA, complete cds, clone Sm51

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1583 A		1448	U07201	Alanine and aspartate metabolism, Nitrogen metabolism	Asparagine synthetase	Asparagine synthetase
1598 C,J		1722	NM_024134		DNA-damage inducible transcript 3	Rattus norvegicus GADD153 mRNA, complete cds
1610 C		1703	NM_022509			Rattus norvegicus survival motor neuron (smn) mRNA, complete cds
1625 I		1588	NM_012924		Cell surface glycoprotein CD44 (hyaluronate binding protein)	Cell surface glycoprotein CD44 (hyaluronate binding protein)
1641 E		1354	E03428		Peptidylglycine alpha-amidating monooxygenase	Peptidylglycine alpha-amidating monooxygenase
1644 G		208	AA891068		Peptidylglycine alpha-amidating monooxygenase	Peptidylglycine alpha-amidating monooxygenase
1653 G		1222	AI233806		Peptidylglycine alpha-amidating monooxygenase	Peptidylglycine alpha-amidating monooxygenase
1661 B,E		1459	U26397	Inositol phosphate metabolism	HHs:inositol polyphosphate-4-phosphatase, type I, 107KD	Rattus norvegicus inositol polyphosphate 4-phosphatase mRNA, complete cds
1690 A,E		46	AA817829			EST's, Highly similar to MEK binding partner 1 [M.musculus]
1700 P		1486	X03369		tubulin, beta 2	EST's, Highly similar to TBB1_RAT TUBULIN BETA CHAIN [R.norvegicus],Rat mRNA for beta-tubulin T beta15
1727 C,J		482	AF001417			Rattus norvegicus zinc finger protein mRNA, complete cds

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				Bile acid biosynthesis, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Phenylalanine metabolism, Valine, leucine and isoleucine degradation	HHs:hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	Rat mRNA for mitochondrial long-chain 3-ketoacyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, complete cds
1728 E.S		1332	D16479		GTP-binding protein	GTP-binding protein
1749 K		1657	NM_017327		HHs:cytochrome P450, subfamily IVF, polypeptide 2	Rattus norvegicus cytochrome P450 4F6 (CYP4F6) mRNA, complete cds
1753 A		1462	U39208	Prostaglandin and leukotriene metabolism	Calcium channel alpha 1A	Calcium channel alpha 1A
1777 P		1586	NM_012918		Cytochrome P450, subfamily IIIA, polypeptide 3	Cytochrome P450, subfamily IIIA, polypeptide 3
1795 B,K,Q		1392	L24207		Cytochrome P450, subfamily IIIA, polypeptide 3	Cytochrome P450, subfamily IIIA, polypeptide 3
1796 B,K		1392	L24207			ESTs
1802 H		47	AA817841			Rattus rattus guanine nucleotide-releasing protein (mss4) mRNA, complete cds
1805 N		508	A007824			Rat mRNA for alpha-2u globulin-related protein
1809 F		391	AA946503		Protein-tyrosine phosphatase	Protein-tyrosine phosphatase
1841 C,N		1555	NM_012637		Protein-tyrosine phosphatase	Protein-tyrosine phosphatase
1843 N,Q		1555	NM_012637		Protein-tyrosine phosphatase	ESTs, Protein-tyrosine phosphatase
1844 A,N		1555	NM_012637		K-kinogen, differential splicing leads to HMW Kngk, T-kinogen	K-kinogen, differential splicing leads to HMW Kngk, T-kinogen
1854 M		1382	K02814			

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1858 S		1524	Y09333		acyl-CoA thioesterase 1, cytosolic	R.norvegicus mRNA for mitochondrial very-long-chain acyl-CoA thioesterase Rattus norvegicus mRNA for acyl-CoA hydrolase, complete cds
1877 A		1513	X74593	Fructose and mannose metabolism	Sorbitol dehydrogenase	Sorbitol dehydrogenase
1884 L		1340	D50695			Rattus norvegicus mRNA for proteasomal ATPase (Tat-binding protein7), complete cds
1893 P		1495	X51529	Glycerolipid metabolism, Phospholipid degradation, Prostaglandin and leukotriene metabolism	phospholipase A2, group IIA (platelets, synovial fluid)	Rattus norvegicus mRNA for phospholipase A2 precursor, complete cds
1900 A,B,L		48	AA817849			ESTs
1901 L		48	AA817849			ESTs
1903 L		1013	A1177377			ESTs
1919 H		815	A1137856		P450 (cytochrome) oxidoreductase	Rat NADPH-cytochrome P-450 oxidoreductase mRNA, complete cds
1920 H		1397	M10068		P450 (cytochrome) oxidoreductase	Rat NADPH-cytochrome P-450 oxidoreductase mRNA, complete cds
1921 H		1351	E01524		P450 (cytochrome) oxidoreductase	Rat NADPH-cytochrome P-450 oxidoreductase mRNA, complete cds
1929 A		1449	U10357		Hsp.iPYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 2, MITOCHONDRIAL PRECURSOR	Rattus norvegicus pyruvate dehydrogenase kinase 2 subunit p45 (PDK2) mRNA, complete cds
1930 L		410	AA957202			Rattus norvegicus pyruvate dehydrogenase kinase 2 subunit p45 (PDK2) mRNA, complete cds

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1957	K	1628	NM_017060	Glycine, serine and threonine metabolism, Methionine metabolism	Hras-revertant gene 107	Hras-revertant gene 107
1995	N	492	AF038870		HMM:betaine-homocysteine methyltransferase	Rattus norvegicus betaine homocysteine methyltransferase (BHMT) mRNA, complete cds
2006	E	1716	NM_022936			R.norvegicus mRNA for cytosolic epoxide hydrolase
2011	P	1610	NM_013173		Solute carrier family 11 member 2 (natural resistance-associated macrophage protein 2)	Solute carrier family 11 member 2 (natural resistance-associated macrophage protein 2)
2012	P	1610	NM_013173		Solute carrier family 11 member 2 (natural resistance-associated macrophage protein 2)	Solute carrier family 11 member 2 (natural resistance-associated macrophage protein 2)
2013	P	1610	NM_013173		Solute carrier family 11 member 2 (natural resistance-associated macrophage protein 2)	Solute carrier family 11 member 2 (natural resistance-associated macrophage protein 2)
2042	Q,R	721	A101921			ESTs
2043	E,H	1125	A1230171			ESTs
2049	J	417	AA963369			ESTs
2051	S	418	AA963372			ESTs
2055	I	1084	A1227769			ESTs
2101	R	565	A1013667			ESTs
2111	A	750	A103550			ESTs
2113	S	423	AA964275			Rattus norvegicus CDK102 mRNA
2117	R	324	AA925961			ESTs, Weakly similar to AF077030_1
2153	E	1475	U75404			hypothetical 43.2 kDa protein [H.sapiens]
						Rattus norvegicus Na-K-Cl cotransporter (Nkcc1) mRNA, complete cds
						ESTs

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2164R		1223	AI233818			ESTs
2164A		781	AI111413			ESTs
2190S		420	AA964004			ESTs
2196A		776	AI106243			ESTs
2216R		912	AI171745			ESTs
2264A		821	AI144741			ESTs
2280H		421	AA964139			EST
2292E		714	AI101362			ESTs
2310M		587	AI029669			ESTs
2326L		432	AA964892			ESTs, Highly similar to CA14_MOUSE COLLAGEN ALPHA 1(V) CHAIN PRECURSOR [M.musculus]
2335A		424	AA964302			ESTs
2339E		1162	AI231798			ESTs
2342E		425	AA964336			EST
2350D		426	AA964368			ESTs, Highly similar to TGT_HUMAN QUEUINE TRNA- RIBOSYLTRANSFERASE [H.sapiens]
2354L		454	AA997763			ESTs, Highly similar to hypothetical protein [H.sapiens]
2359N		998	AI177029			ESTs, Highly similar to JI0227 protein- tyrosine kinase [M.musculus]
2368N		504	AF095741			Rattus norvegicus MG87 mRNA, complete cds
2372AL		1130	AI230373			ESTs
2373O		428	AA964455			ESTs
2383AE		429	AA964514			ESTs
2457S		431	AA964752			EST
2484AO		761	AI104675			ESTs

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2505	A,G	1549	NM_012597	Glycerolipid metabolism	Lipase, hepatic	Lipase, hepatic
2506	E	524	AI009341			ESTs
2532	A	975	AI176590			ESTs
2536	A	978	AI176616			ESTs
2555	B,C,Q	1590	NM_012967		Intercellular adhesion molecule 1	Intercellular adhesion molecule 1
2569	A,C,F,K,R	435	AA965122			ESTs
2576	A	226	AA891884			ESTs
2587	G	1170	AI232103			ESTs
2594	L	1241	AI234843			ESTs, Moderately similar to Similarity to Yeast LPG22P protein [C.elegans]
2615	C,J	1109	AI293318			ESTs
2628	J	1551	NM_012603		Avian myelocytomatosis viral (v-myc) oncogene homolog	Avian myelocytomatosis viral (v-myc) oncogene homolog
2629	J	1551	NM_012603		Avian myelocytomatosis viral (v-myc) oncogene homolog	Avian myelocytomatosis viral (v-myc) oncogene homolog
2655	B,N,Q	343	AA943886			Rattus norvegicus protein kinase SNK (Snk) mRNA, complete cds
2667	G	1588	NM_012766		Tocopherol transfer protein alpha	Tocopherol transfer protein alpha
2691	R	434	AA965075			ESTs
2696	A	1737	NM_022515			R.norvegicus (Sprague Dawley) mRNA for ribosomal protein L24
2727	H	252	AA892918			ESTs
2736	Q	1537	NM_012519		Ca++/calmodulin-dependent protein kinase II, delta subunit	Ca++/calmodulin-dependent protein kinase II, delta subunit
2744	I	1347	D87991			ESTs, Highly similar to UGTrel1
2757	L	456	AA997851			[M.musculus] ESTs
2762	A	350	AA944165			ESTs, Highly similar to C10 [M.musculus]

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2763 E		1173	AI232269			ESTs
2781 I		50	AA817925			ESTs
2788 J		939	AI175513			Rattus norvegicus mRNA for phocein protein
2799 A		568	AI013778			ESTs
2801 F		1345	D85435			Rattus norvegicus mRNA for protein kinase C delta-binding protein, complete cds
2802 F		1345	D85435			Rattus norvegicus mRNA for protein kinase C delta-binding protein, complete cds
2803 L		437	AA996451			ESTs
				Butanoate metabolism, Synthesis and degradation of ketone bodies, Valine, leucine and isoleucine degradation		
2813 S		365	AA945052		Hm:3-hydroxy-3-methylglutaryl-Coenzyme A lyase	R-norvegicus mRNA for 3-hydroxy-3-methylglutaryl CoA lyase
2818 C,D,F		1055	AI179144			ESTs
2838 D		655	AI070511			ESTs, Highly similar to G/A [M.musculus]
2853 I		1579	NM_012838		Cystatin beta	Cystatin beta
2854 I		1579	NM_012838		Cystatin beta	Cystatin beta
2868 E		1171	AI232209			ESTs
2897 C,D		51	AA818039			ESTs
2901 A		603	AI043752			ESTs
2905 A,B		438	AA996727			ESTs
2911 A		597	AI030835			ESTs
2915 R		439	AA996782			ESTs
2932 R		1204	AI233288			ESTs

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2933	E	1665	NM_019204			ESTs, Highly similar to beta-site APP cleaving enzyme [R.norvegicus]
2938	C	440	AA996883			ESTs
2993	A	971	AI176492			ESTs, Highly similar to AF188297_1 TGF-beta receptor binding protein [M.musculus]
3023	G	885	AI170795			ESTs
						EST, Weakly similar to CBPB_RAT CARBOXYPEPTIDASE B PRECURSOR [R.norvegicus]
3062	D	468	AA998857			ESTs
3073	A,E,O	1213	AI233494			ESTs
3074	A,E,O	1213	AI233494			ESTs
3075	A,O	1213	AI233494			ESTs
					HHs: signal transducer and activator of transcription 1, 91kD	Rattus norvegicus signal transducer and activator of transcription 1 (Stat1) mRNA, complete cds
3080	H	242	AA892553			ESTs
3091	E	1260	AI236027		HHs: NADH dehydrogenase (ubiquinone) Fe-S protein 3 (30kD) (NADH-coenzyme Q reductase)	ESTs, Highly similar to NADH-ubiquinone oxidoreductase NDUF53 subunit [H.sapiens]
3099	S	1113	AI229680	Oxidative phosphorylation, Ubiquinone biosynthesis		ESTs, Moderately similar to AF151841_1 CGI-83 protein [H.sapiens]
						ESTs
3121	A,B,E	510	AI008160			ESTs
3131	A	256	AA893032			ESTs
3138	I	1047	AI178850			ESTs
3139	J	540	AI010618			ESTs
3143	E,H	1180	AI232408			ESTs
3145	A	444	AA997237			EST
3175	S	447	AA997414			ESTs

TABLE 1					Document Number 1650775	
GLUC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
3189	A		448 AA997438			ESTs, Moderately similar to LDL receptor member LR3 [M.musculus]
3203	C		1624 NM_017039		Protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	Protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform
3207	A		449 AA997466			ESTs
3219	E		767 AI105065			ESTs, Highly similar to PNAD_MOUSE PROTEIN N-TERMINAL ASPARAGINE AMIDOHYDROLASE [M.musculus]
3233	L		53 AA818105			ESTs, Moderately similar to Unknown gene product [H.sapiens]
3250	M		455 AA997765			Rattus norvegicus fibrillin-1 mRNA, complete cds
3253	F		1652 NM_017282		proteasome (prosome, macropain) subunit, alpha type 5	proteasome (prosome, macropain) subunit, alpha type 5
3260	S		571 AI013875			ESTs
3266	L		915 AI171948			ESTs
3279	S		747 AI103224			ESTs, Weakly similar to putative short-chain dehydrogenase/reductase [R.norvegicus]
3280	C		1083 AI227699			ESTs
3292	M,N		1325 D00753			Rat mRNA for contrapsin-like protease inhibitor related protein (CPI-26)
3365	A,B		518 AI008919			ESTs
3381	K		254 AA892993			ESTs
3418	A,C,D		936 AI175475			ESTs, Highly similar to NHPX_RAT NHP2/RS6 FAMILY PROTEIN
3430	J		1441 S85184		Cathepsin L	YELO26W HOMOLOG [R.norvegicus] Cathepsin L

TABLE 1					Document Number: 1650775	
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
3439 S		255	AA893000			ESTs, Highly similar to KIAA0564 protein [H.sapiens]
3452 M,N		452	AA997721			Rattus norvegicus orphan chemokine receptor mRNA, complete cds
3486 H		869	AI170313			ESTs
3504 A,B		760	AI104659			Rattus norvegicus mRNA for R-RCD1, complete cds
						ESTs, Highly similar to ZO1_MOUSE TIGHT JUNCTION PROTEIN ZO-1 [M.musculus]
3510 K		963	AI176423			choline/ethanolamine kinase
3573 S		1639	NM_017177	Glycerolipid metabolism	choline/ethanolamine kinase	Rat signal peptidase mRNA, complete cds
3549 H,I		1385	L11319			EST
3558 S		463	AA98461			ESTs, Weakly similar to RET1_RAT RETINOL-BINDING PROTEIN I, CELLULAR [R.norvegicus]
3570 O		464	AA98510			ESTs
3587 J		1078	AI180253			
						Rattus norvegicus gene for hepatocarcinogenesis-related transcription factor (HTF), complete cds
3617 N		1259	AI236021			ESTs, Weakly similar to JC1450 fibroblast growth factor receptor 4 - rat [R.norvegicus]
3626 P		950	AI176031			ESTs, Highly similar to Opa-interacting protein OIP2 [H.sapiens]
3631 S		302	AA924460			ESTs
3660 B		467	AA988333			EST
3708 M		469	AA999060			

TABLE 1						Document Number 1650775	
GLQC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title	
3710 B,Q		470	AA999064			ESTs	
3713 A,N		791	AI112571			ESTs	
3720 S		471	AA999138			ESTs	
3722 N		457	AA997979			ESTs	
3730 N		460	AA998234			EST	
3743 S		1335	D30666			Rat mRNA for brain acyl-CoA synthetase II, complete cds	
3749 P		461	AA998276			EST	
3776 Q		1679	NM_019354		Uncoupling protein 2, mitochondrial	Uncoupling protein 2, mitochondrial	
3803 L,R		884	AI170773			Rattus norvegicus 250 kDa estrous-specific protein mRNA, partial cds	
3816 J		1219	AI233729			ESTs, Highly similar to PSD5_HUMAN 26S PROTEASOME SUBUNIT S5B [H.sapiens]	
3822 A		288	AA900863			ESTs, Weakly similar to nuclear RNA helicase [R.norvegicus]	
3823 A		1196	AI233147			ESTs, Weakly similar to nuclear RNA helicase [R.norvegicus]	
3831 C,J		1525	Y12635	Oxidative phosphorylation	HmM:ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta 56/58 kDa, isoform 2	R norvegicus mRNA for vacuolar adenosine triphosphatase subunit B	
3846 O		658	AI070895			ESTs, Weakly similar to acyl-CoA dehydrogenases and epoxide hydrolases [C.elegans]	
3849 A		567	AI013745			ESTs, Moderately similar to CGI-147 protein [H.sapiens]	
3916 A,F		865	AI169947			ESTs	
3917 B		1194	AI232970			ESTs	
3929 O		270	AA894233			ESTs	

TABLE 1				Document Number: 1650775		
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
3934 A		544	A011510			ESTs
						ESTs, Highly similar to IF2B_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT [H.sapiens]
3959 A		292	AA901338			ESTs
3969 A		1001	A1177055			ESTs
3972 Q		300	AA924307			ESTs
3976 E		61	AA818264			ESTs, Weakly similar to similar to GTPase-activating proteins [H.sapiens]
3981 A		554	A012235			ESTs
3995 A		545	A011678			ESTs
4017 A		63	AA818287			ESTs
4026 B,Q		1225	A1233835			ESTs
4048 I		139	AA851814			Rattus norvegicus osteocalcin mRNA, complete cds
4049 I		784	A1112012			Rattus norvegicus osteocalcin mRNA, complete cds
4082 O		624	A045256			ESTs
4084 A		512	A008504			ESTs
				Glycolysis/ Gluconeogenesis		R.norvegicus phosphoglycerate mutase B isozyme (PGAM) mRNA, complete cds
4092 L		1095	A028723		HHs phosphoglycerate mutase 1 (brain)	ESTs
4097 I		1037	A1178635			ESTs
4119 J		720	A101901			ESTs
4127 H		1057	A1179206			ESTs
4143 A		786	A112107			ESTs
4157 E		525	A009481			ESTs, Weakly similar to putative [C.elegans]
4168 E		527	A009654			ESTs

TABLE 1					Document Number: 1650775	
GLCC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
4178 I		170	AA859536			ESTs
4179 A,C,E,R		1132	AI230431			ESTs
4183 A,C,D,E,F,I		923	AI172274			ESTs, Weakly similar to I37195 AU-specific RNA-binding protein / enoyl-CoA hydratase [H.sapiens]
4199 G		1425	M83143		Sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase)	Rat beta-galactoside-alpha 2,6-sialyltransferase mRNA
4207 F		371	AA945591			ESTs, Weakly similar to JC5105 stromal cell-derived factor 2 - mouse [M.musculus]
4224 G		1415	M31322			Rat sperm membrane protein (YWK-II) mRNA, 3' end
4231 R		1159	AI231763			Rattus norvegicus late gestation lung 2 protein (Lg2) mRNA, complete cds
4234 H		1685	NM_021577			Rattus norvegicus mRNA for AIF-C1, complete cds
4250 B		76	AA818700			ESTs
4271 S		321	AA925603			ESTs, Moderately similar to AF153605_1 androgen induced protein [H.sapiens]
4272 S		1152	AI231309			ESTs, Moderately similar to AF153605_1 androgen induced protein [H.sapiens]
4281 A,G		1663	NM_019192		selenoprotein P, plasma, 1	selenoprotein P, plasma, 1
4290 S		1323	AJ224120			Rattus norvegicus peroxisomal membrane protein Pmp26p (Peroxin-11)
4291 A,H		79	AA818741			ESTs

TABLE 1					Document Number: 1650775	
GLCC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
4312 K		480	AB010635			Rattus norvegicus bile salt export pump carboxylesterase precursor, complete cds
4314 G,M		483	AF010597			Rattus norvegicus bile salt export pump (sgp) mRNA, complete cds
4318 F		474	AB005900			Rattus norvegicus mRNA for endothelial receptor for oxidized low-density lipoprotein, complete cds
4327 I		498	AF063447			Rattus norvegicus nuclear RNA helicase mRNA, complete cds
4330 A,C,D,E		80	AA818747			Rattus norvegicus stromal cell-derived factor-1 gamma mRNA, complete cds
4348 E		874	AI170447			Rattus norvegicus mRNA for norepinephrine transporter b (rNETb), complete cds
4360 A		1358	H31813			ESTs
4371 E		295	AA924196			ESTs
4426 I		3	AA685974			ESTs
4438 S		2	AA684919			ESTs
4440 A,O		1189	A232643			ESTs
4473 A		229	AA891965			ESTs
4504 Q		1725	NM_024159			Rattus norvegicus DOC-2 p59 isoform mRNA, complete cds
4520 O		751	AI103894	Oxidative phosphorylation,	HHs:NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2	ESTs, Moderately similar to NADH-ubiquinone oxidoreductase subunit Cl-
4553 A,C		999	AI177038	Ubiquinone biosynthesis	(8kD, B8)	B8 [H.sapiens]
4576 K		1049	AI178872			ESTs

TABLE 1					Document Number: 1650775	
GLCC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
4588	K		477 AB009636			Rattus norvegicus mRNA for phosphoinositide 3-kinase, complete cds
4592	C,D		1680 NM_019356		eukaryotic translation initiation factor 2, subunit 1 (alpha)	subunit 1 (alpha)
4610	E		1075 AI179991			ESTs
4650	G		718 AI101582			ESTs
4670	A,N		1217 AI233714			ESTs
4674	O		279 AA899847			EST
4679	L					ESTs, Highly similar to IRF3, MOUSE INTERFERON REGULATORY FACTOR 3 [Musculus]
4719	A		585 AI029847			ESTs
4725	L		1087 AI228265			ESTs
4759	E		282 AA900290			ESTs
4781	C,D		285 AA900553			ESTs
4856	I		1228 AI233925			ESTs
4868	A		752 AI103708			ESTs
4892	P		882 AI170763			ESTs
4914	A		611 AI044292			ESTs
4929	E		785 AI112086			ESTs
			296 AA924236			EST
4931	S					ESTs, Moderately similar to unknown
4933	A,E,P		297 AA924261			[H.sapiens]
4937	A,L		299 AA924301			EST
			1294 AI237189			ESTs
4940	S					Rattus norvegicus rap7a mRNA, complete cds
			1738 NM_022526			

TABLE 1					Document Number 1650775	
GLQC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
4944 A.F		301	AA924405			ESTs, Moderately similar to
4951 A		519	AI009026			NO56_HUMAN NUCLEOLAR PROTEIN
4952 C.J		86	AA818907			NOP56 [H.sapiens]
						ESTs
						ESTs
						ESTs, Moderately similar to megakaryocyte stimulating factor [H.sapiens]
4959 M		795	AI113008			ESTs
5008 A.C		88	AA818921			EST
5018 L		306	AA924767			ESTs, Weakly similar to MRJ [M.musculus]
5020 E		307	AA924768			ESTs
5027 A		308	AA924793			ESTs
5038 E		846	AI169239			ESTs
5046 A.L		1303	AI237855			ESTs
						ESTs, Weakly similar to TTHY_RAT TRANSXYRETIN PRECURSOR [R.norvegicus]
5052 R		1270	AI236302			ESTs
5059 Q		1288	AI236947			ESTs
5091 E		699	AI073092			ESTs
5110 E.M		317	AA925274			ESTs
5111 E		397	AA955729			EST, ESTs
				Glycolysis/ Gluconeogenesis, Purine metabolism, Pyruvate metabolism		
5175 A		90	AA818951		Pyruvate kinase, muscle	Pyruvate kinase, muscle
5219 A		322	AA925807			ESTs
5235 F		829	AI145569			ESTs, Moderately similar to BcDNA GH02974 [D.melanogaster]

TABLE 1				Document Number 1650775		
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
5291	M	1190	AI232700	Aminoacyl-tRNA biosynthesis, Glutamate metabolism		ESTs
5331	I	91	AA818996			ESTs, Moderately similar to SYQ_HUMAN GLUTAMINYL-TRNA SYNTHETASE [H.sapiens]
5339	E,M	911	AI171727	Nicotinate and nicotinamide metabolism	HHs:glutaminyl-tRNA synthetase	ESTs, Weakly similar to PNMT [R.norvegicus]
5381	R	1038	AI178734			ESTs
5384	A,B,F	207	AA891041			ESTs
5434	E	1380	K01878		Proopiomelanocortin, beta (endorphin, beta)	Rat proopiomelanocortin (POMC) gene
5437	F	407	AA956910			ESTs
5461	A	613	AI044338			EST
5464	B,O	614	AI044345			ESTs, Highly similar to AF172275_1 FUS2 [M.musculus]
5489	C,J	914	AI171795			ESTs
				Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism		
5492	G	1336	D38061	Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism	UDP-glucuronosyltransferase 1 family, member 1	ESTs,UDP-glucuronosyltransferase 1 family, member 1
5493	G,O	1433	S56936	Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism	UDP-glucuronosyltransferase 1 family, member 1	ESTs,UDP-glucuronosyltransferase 1 family, member 1

TABLE 1				Document Number: 1650775		
GLQC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
						ESTs, Weakly similar to NUML_MOUSE NADH-UBIQUINONE OXIDOREDUCTASE MLRQ SUBUNIT [M.musculus] EST ESTs
5504 D		1165	AI231805			
5518 S		617	AI044550			
5565 S		377	AA945879			
						ESTs
5602 S		1187	AI232611			ESTs, Weakly similar to mitochondrial very-long-chain acyl-CoA thioesterase [R.norvegicus] ESTs
5608 R		93	AA819041			
5616 M.S		1731	NM_019143		Fibronectin 1	Fibronectin 1
5622 A		1731	NM_019143		Fibronectin 1	Fibronectin 1
5687 P		705	AI101006			ESTs
5696 L		621	AI045116			ESTs
					P-glycoprotein 2/ multidrug resistance 1b, P-glycoprotein/multidrug resistance 1	P-glycoprotein/multidrug resistance 1
5733 C		1424	M81855			ESTs, Moderately similar to DYNK_HUMAN DYNACTIN, 50 KD ISOFORM [H.sapiens]
5740 L		680	AI072092			proteasome (prosome, macropain) subunit, alpha type 2
5748 A		1650	NM_017279			proteasome (prosome, macropain) subunit, alpha type 2
5749 A.H		1650	NM_017279			proteasome (prosome, macropain) subunit, alpha type 2
5754 L.R		133	AA850738			ESTs
						ESTs, Weakly similar to DRAL [R.norvegicus]
5780 C.D		1019	AI177869			ESTs
5794 C		1212	AI233480			ESTs
5795 E		626	AI045441			ESTs

TABLE 1					Document Number: 1650775	
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
5813 A		1026	A178231			ESTs
5820 J		1285	A1236771			ESTs
5824 K		5824	A1045555			EST
5863 A		95	AA819111			ESTs
5867 A,C,D		158	AA858953	Alanine and aspartate metabolism, Aminoacyl-tRNA biosynthesis	HHs:asparaginyl-tRNA synthetase	ESTs, Highly similar to SYN_HUMAN ASPARAGINYL-TRNA SYNTHETASE, CYTOPLASMIC [H.sapiens]
5885 I		1322	A1223184			Rattus norvegicus mRNA for DORA protein
5887 S		1053	A179099			ESTs, Moderately similar to Vanin-1
5899 A,D,F		867	A170038		vanin 1	[M.musculus]
5920 G		843	A169163			ESTs
5923 A		65	AA818355			ESTs
5926 C		1017	A177638			ESTs, Moderately similar to M phase phosphoprotein 10 [H.sapiens]
5930 E		42	AA817688			ESTs
5932 J		756	A104254			ESTs
5934 A,F		43	AA817695			ESTs, Highly similar to 2008147C protein RAKd [R.norvegicus]
5937 J		908	A171684			ESTs
5943 A		1005	A177105			ESTs
5953 H		893	A171231			Rattus norvegicus amino acid transporter system A (ATA2) mRNA, complete cds
5966 H		89	AA818947			ESTs
5993 R		820	A144612			ESTs
5998 G		1317	A1639501			ESTs
6003 E		54	AA818107			ESTs

TABLE 1					Document Number: 1650775	
GLC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
6007 A		55	AA818123			ESTs
6012 D		56	AA818139			ESTs
6013 N		1634	NM_017096		C-reactive protein	C-reactive protein
6015 A.O		57	AA818158			ESTs
6016 A.C.D		58	AA818163			EST
6017 A		1676	NM_019292	Nitrogen metabolism	carbonic anhydrase 3	carbonic anhydrase 3
6018 E.N		96	AA819140	Nitrogen metabolism	carbonic anhydrase 3	carbonic anhydrase 3
6026 E		59	AA818211			EST
6032 E		60	AA818258			ESTs
6033 A		1195	AI233081			ESTs
6037 A		64	AA818288			ESTs
6039 D		330	AA942716			ESTs, Highly similar to HN1
6060 A.O		77	AA818702			[M.musculus]
6066 E		83	AA818781			ESTs
6072 A.B.E.F		1093	AJ228630			ESTs
6085 C		916	AI171990			ESTs, Weakly similar to Similarity to
6101 R		881	AI170752			litospem LEC14B protein [C.elegans]
6132 A.C.D		94	AA819055			ESTs, Moderately similar to axonemal
						dynem heavy chain [H.sapiens]
						ESTs
						EST
6143 A.C		771	AI105167			ESTs, Moderately similar to selenium-
6151 G		98	AA819199			binding protein [H.sapiens]
						EST
6153 G		203	AA875531			Rattus norvegicus pro-alpha-2(I)
6155 G						collagen (col1a2) mRNA, complete cds
						Rattus norvegicus pro-alpha-2(I)
						collagen (col1a2) mRNA, complete cds
6188 E		82	AA818774			ESTs

TABLE 1				Document Number:1650775		
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc.ID	Pathways	Known Gene Name	UniGene Cluster Title
6189	B,E,G	1023	A178027			ESTs, Weakly similar to GTP_RAT
6190	A	107	AA819812			GLUTATHIONE S-TRANSFERASE P [R.norvegicus]
6193	I	1161	A1231797			ESTs
6198	M	109	AA819840			ESTs
6200	P	110	AA819853		HHs:lymphotoxin beta (TNF superfamily, member 3)	ESTs, Highly similar to TNFC_MOUSE
6213	N	726	A102190			LYMPHOTOXIN-BETA [M.musculus]
6222	N	68	AA818474			ESTs
6226	A	70	AA818521			ESTs
6236	B,E,P	75	AA818627			EST, Moderately similar to ISI1_RAT
						INSULIN-INDUCED PROTEIN 1 [R.norvegicus]
						ESTs, Weakly similar to B39066 proline-rich protein 15 - rat [R.norvegicus]
6272	L	875	A170617			ESTs
6291	H	822	A1144797			ESTs
6292	S	422	AA964181			ESTs
6295	N	103	AA819672			EST
6321	A,J	712	A101256			ESTs, Weakly similar to AIF-C1 [R.norvegicus]
6322	A	85	AA818801			EST
6330	H	873	A1170426			ESTs
6366	A,E,H	152	AA858716			Rattus norvegicus mRNA for signal peptidase 21kDa subunit, complete cds
6380	A,C,D	153	AA858758			ESTs, Weakly similar to dJ413H6.1.1 [H.sapiens]

TABLE 1					Document Number: 1650775	
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
6409 E		156	AA858910			ESTs
6410 A		157	AA858926			ESTs
6431 K,P		159	AA859085			EST
6439 S		636	AI058436			ESTs
6440 R		160	AA859130			ESTs
6443 A		161	AA859150			ESTs
6473 A		1002	AI177091		Fibrinogen, gamma polypeptide	Fibrinogen, gamma polypeptide
6477 N		1371	J00735		Fibrinogen, gamma polypeptide	Fibrinogen, gamma polypeptide
6479 K		860	AI168680		Fibrinogen, gamma polypeptide	ESTs
6532 B,Q		1232	AI234105			ESTs, Moderately similar to hypothetical protein [H.sapiens]
6533 E		155	AA858852			ESTs
6541 O		740	AI102905			ESTs
6549 O		949	AI176002	Folate biosynthesis		ESTs, Highly similar to S65755 tetrahydrofolylpolyglutamate synthase [M.musculus]
6553 S		594	AI030271		Folypolyglutamate synthase	ESTs
6554 A		505	AF097723			Rattus norvegicus liver annexin-like protein (LAL) mRNA, complete cds
6582 L		910	AI171726			ESTs, Weakly similar to ESR1_RAT ESTROGEN RECEPTOR [R.norvegicus]
6585 F		1685	NM_022266			Rattus norvegicus mRNA for connective tissue growth factor, complete cds
6604 A,O		1104	AI229192			ESTs

TABLE 1			Document Number: 1650775	
GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name
			Butanoate metabolism, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Lysine degradation, Tryptophan metabolism, Valine, leucine and isoleucine degradation	
6613 A,F	117	AA848758		HMn:hydroxyl-Coenzyme A dehydrogenase
				Rattus norvegicus L-3-hydroxyacyl-CoA dehydrogenase precursor (HAD) mRNA, complete cds; nuclear gene for mitochondrial product
				ESTs, Weakly similar to putative type III alcohol dehydrogenase
6615 A	335	AA942889		[D.melanogaster]
6632 A	1246	AI235277		ESTs
6633 A,N	1098	AI228931		ESTs
6640 A	716	AI101500		ESTs
6667 K	905	AI171646		ESTs
				Rattus norvegicus mRNA for N-cadherin, complete cds
6673 E	612	AI044325		ESTs
6676 L	143	AA851967		ESTs
6677 S	542	AI011471		ESTs
6682 A	1168	AI232065		ESTs
6686 R	952	AI176130		ESTs
				ESTs, Highly similar to methyl-CpG binding domain-containing protein MBD3 [M.musculus]
6761 A	513	AI008699		ESTs
6789 O,R	459	AA998207		ESTs
6796 C	735	AI102753		ESTs
6798 E	857	AI169619		ESTs
6801 A,E,K	536	AI010316		ESTs
6804 E	509	AI007877		ESTs

TABLE 1					Document Number 1650775	
QLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title	
6814 E	717	A101534			EST.Rattus norvegicus Mdk mRNA for midkine, complete cds	
6820 A,D	1133	A230439			ESTs	
6821 E,L	990	A1176841			ESTs	
6824 A,C,D,F,I	104	AA819709			ESTs	
6825 A,B,Q,S	631	A045972			ESTs	
6855 A,L	899	A171370			ESTs	
6861 H,R	995	A176970			ESTs	
6879 I	907	A1171674			ESTs	
6892 J	33	AA800551			Rattus norvegicus DnaJ-like protein (RDJ1) mRNA, complete cds	
			Pantothenate and CoA biosynthesis, Pyrimidine metabolism, beta-Alanine metabolism		Rattus norvegicus mRNA for dihydropyrimidine dehydrogenase, complete cds	
6911 D	1343	D85035		HHs:dihydropyrimidine dehydrogenase	ESTs	
6919 N	537	A010461			ESTs	
6975 O	953	A176229			ESTs, Weakly similar to Dreg-2 protein [D.melanogaster]	
7003 A,L	593	A030259			ESTs, Weakly similar to TERA_RAT TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE [R.norvegicus]	
7036 C,J	1164	A231801			ESTs	
7056 B,M	543	A011503	Fructose and mannose metabolism, Glycolysis/ Gluconeogenesis, Pentose phosphate cycle			
7062 A	1533	NM_012495	Aldolase A, fructose-bisphosphate		Aldolase A, fructose-bisphosphate	

TABLE 1 Document Number: 1650775

GLQC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
7063	A,C,D	1533	NM_012495	Fructose and mannose metabolism, Glycolysis/ Gluconeogenesis, Pentose phosphate cycle	Aldolase A, fructose-bisphosphate	Aldolase A, fructose-bisphosphate
7064	A,C	1533	NM_012495	Fructose and mannose metabolism, Glycolysis/ Gluconeogenesis, Pentose phosphate cycle	Aldolase A, fructose-bisphosphate	Aldolase A, fructose-bisphosphate
7111	R	108	AA819816			ESTs
7113	A	868	AI170260			ESTs
7122	Q	809	AI137468			ESTs
7161	C	1209	AI233407			ESTs
7176	Q	1306	AI639029			ESTs
7196	P	1585	NM_012904		Annexin 1 (p35) (Lipocortin 1)	Annexin 1 (p35) (Lipocortin 1)
7199	C,D	562	AI013044			ESTs
7225	M	564	AI013657			ESTs
7243	A,C	1218	AI233717			ESTs
7262	D,L	946	AI175833			ESTs
7271	C	1115	AI229739			ESTs
7295	S	572	AI013676			ESTs
7299	A	573	AI013911			ESTs, Weakly similar to CIRP [R:norvegicus]
7301	J	111	AA819854			ESTs
7362	A	577	AI028973			ESTs, Weakly similar to AF165802.1 RNA-binding protein SiahBP [R:norvegicus]
7362	L	578	AI029026			ESTs
7403	C,D	579	AI029212			EST

TABLE 1						Document Number: 1650775
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
7414	C,D	813	AI137586			ESTs, Highly similar to IMB3_HUMAN IMPORTIN BETA-3 SUBUNIT [H.sapiens]
7420	S	580	AI029291			ESTs, Highly similar to CtpX-like protein [H.sapiens]
7451	E,N	581	AI029450			ESTs, Moderately similar to SYEP_HUMAN MULTIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE [H.sapiens]
7497	O	849	AI169302	Sphingophospholipid biosynthesis	HMM:sphingomyelin phosphodiesterase 1, acid lysosomal	ESTs, Moderately similar to sphingomyelin phosphodiesterase 1, acid lysosomal [H.sapiens]
7517	S	582	AI029709			ESTs
7528	H	749	AI103548			ESTs, Highly similar to AF115778_1 short coiled coil protein SCOCO [M.musculus]
7531	A	1298	AI237614			ESTs
7537	E	584	AI029829			ESTs
7552	E,G,I	629	AI045802			EST
7582	A	588	AI029996			ESTs
7584	O	601	AI043724			ESTs
7586	L	589	AI030024			ESTs
7602	I	1320	AJ001929			Rattus norvegicus mRNA for of CBP-50 protein
7617	A	591	AI030170			ESTs
7665	F	596	AI030668			ESTs
7681	A	595	AI030449			ESTs, Moderately similar to methyltransferase related protein [M.musculus]

TABLE 1				Document Number: 1650775		
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
7684	O	592	A1030242			ESTs
7690	I	1700	NM_022284			Rattus norvegicus uroguanylin mRNA, complete cds
7697	A,M	992	A1176942			ESTs
7743	P	651	A1070233			ESTs
7784	A	1570	NM_012789		Dipeptidyl peptidase 4	Dipeptidyl peptidase 4
7785	A,C	1570	NM_012789		Dipeptidyl peptidase 4	Dipeptidyl peptidase 4
7806	J	67	AA818421			ESTs
7858	M,P	599	A1043654			EST
7868	A	711	A1101229			ESTs
				Aminoacyl-tRNA biosynthesis, Arginine and proline metabolism		ESTs, Moderately similar to SYR_HUMAN ARGINYL-TRNA SYNTHETASE [H.sapiens]
7887	C,D	823	A1144832		HHs:arginyl-tRNA synthetase	SYR_HUMAN ARGINYL-TRNA SYNTHETASE [H.sapiens]
				Aminoacyl-tRNA biosynthesis, Arginine and proline metabolism		ESTs, Moderately similar to SYR_HUMAN ARGINYL-TRNA SYNTHETASE [H.sapiens]
7888	A,C,D	1215	A1233583		HHs:arginyl-tRNA synthetase	ESTs, Weakly similar to FIBA_RAT FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR [R.norvegicus]
7892	F	1102	A1229172			EST
7893	A	604	A1043761			ESTs
7903	A,E,F	605	A1043805			ESTs
7916	E	606	A1043855		HMm:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisiae)	ESTs, Highly similar to sterol-C5-desaturase [M.musculus]
7918	A	1069	A1179750			ESTs
					HHs:UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase	R.norvegicus mRNA for UDP-N-acetyl-D-glucosamine-2-epimerase
7927	A,H,O	831	A1145931		Aminosugars metabolism	

TABLE 1					Document Number 1650775	
GLQC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
7935 C		607	A1043945	Porphyrin and chlorophyll metabolism	Hm:ferrochelatase	ESTs
7936 A		202	AA875495			ESTs
7967 L		1124	A1230134	Purine metabolism	Hh:adenylate cyclase 9	ESTs
						EST, Weakly similar to putative integral membrane transport protein [R.norvegicus]
8017 P		633	A1058341			ESTs
8053 K		932	A1175033			ESTs
8054 R		1099	A1228959			ESTs
8079 B,M,Q		637	A1058581			ESTs
						ESTs, Moderately similar to PROP_MOUSE PROPERDIN [M.musculus]
8107 G		1318	A1639534		Protein tyrosine phosphatase, gamma (provisional HGM11 symbol)	ESTs
8124 E		742	A1103071			Rattus norvegicus protein-tyrosine phosphatase (SHP-1) mRNA, complete cds
8152 I		1478	U77038		Hm:hemopoietic cell phosphatase	ESTs
8173 E		450	AA997699			ESTs
8177 S		638	A1058603			ESTs
						Rat ferritin light chain subunit, mRNA, Rattus norvegicus kynurenine aminotransferase/glutamine transaminase K (Kat) gene, complete cds
8215 L		909	A1171692			ESTs
8273 P		765	A1104908			EST, Weakly similar to hypothetical protein [H.sapiens]
8274 B		641	A1059270			ESTs
8310 P		1048	A1178868			

TABLE 1				Document Number: 1650775		
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
8314 J		642	AI059386			ESTs
				Alanine and aspartate metabolism, Purine metabolism	Hm:adenylosuccinate synthetase 1, muscle	ESTs, Highly similar to PUA1 MOUSE ADENYLOSUCCINATE SYNTHETASE, MUSCLE ISOZYME [M.musculus]
8315 S		643	AI059389			ESTs, Moderately similar to microsomal glutathione S-transferase 3 [H.sapiens]
8317 A,E		234	AA892234	Glutathione metabolism		EST
8366 G		645	AI059543			ESTs
8387 A		962	AI176365			ESTs
8477 A		1056	AI179167			ESTs
8515 N		127	AA849917			ESTs
8522 M,P		647	AI060071			ESTs
8549 A,F,H		1216	AI233639			ESTs
8592 G		1364	H33491			Rattus norvegicus sterol delta 8-isomerase (RSI) mRNA, complete cds
8597 B,H		72	AA818593			Rattus norvegicus phosphatidate phosphohydrolase type 2 mRNA, complete cds
8600 A		640	AI058956			ESTs
8630 A		529	AI009677			ESTs
						ESTs
8661 J		73	AA818604		Heat shock protein 70-1	Rattus norvegicus heat shock protein 70 (HSP70) mRNA, complete cds
8662 J		115	AA848563		Heat shock protein 70-1	Rattus norvegicus heat shock protein 70 (HSP70) mRNA, complete cds
8663 J		1527	Z27118		Heat shock protein 70-1	(HSP70) mRNA, complete cds

TABLE 1				Document Number: 1650775		
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
8664 J		1530	Z75029		Heat shock protein 70-1	ESTs Rattus norvegicus heat shock protein 70 (HSP70) mRNA, complete cds
8665 J		675	A1071965		Heat shock protein 70-1	ESTs Rattus norvegicus heat shock protein 70 (HSP70) mRNA, complete cds
						ESTs, Weakly similar to putative peroxisomal 2,4-dienoyl-CoA reductase [R.norvegicus]
8692 A		610	A1044247			ESTs
8700 E,M		634	A1058388			ESTs, Weakly similar to DnaJ homolog 2 [R.norvegicus]
8709 R		1185	A1232534			ESTs
8715 N		648	A1069920			ESTs
8728 R		74	AA818615			ESTs
8730 H		1028	A1178483			ESTs
8735 H		697	A1073047			Rattus norvegicus clone P12 unknown mRNA
						ESTs, Weakly similar to thyroid hormone responsive protein [R.norvegicus]
8766 A		549	A1012085			ESTs
8820 S		650	A1070152			Nucleolin
8829 A		1567	NM_012749		Nucleolin	ESTs
8864 P		652	A1070319			ESTs
8872 G,K		134	AA851050			ESTs
8880 A		824	A1144936			ESTs
						ESTs, Highly similar to Ki antigen [M.musculus]
8886 D		1221	A1233766			ESTs
8905 K		790	A1112511			ESTs
8928 I		212	AA891221			ESTs

TABLE 1				Document Number: 1650775		
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
8946 A		656	A1070611			ESTs
						Rattus norvegicus initiation factor 2 associated 67 kDa protein (p67) mRNA, complete cds
8984 J		1735	NM_022539		Hsp:METHIONINE AMINOPEPTIDASE 2	ESTs
8993 R		948	A1175997			EST
9012 A		657	A1070879			ESTs
9015 K		1239	A1234810			EST
9016 A,B,C,D,E		659	A1070903			ESTs
9053 A		249	AA892861			ESTs
9063 A		1197	A1233162			ESTs
9072 G		942	A1175635			ESTs
9079 P		667	A071251			ESTs
		9128	L 903	A1171611		ESTs
9148 B		516	A1008813			ESTs
9164 H		1565	NM_012726		Spinocerebellar ataxia type 1	ESTs
9166 E		807	A1137406			ESTs
9170 E		993	A1176947			ESTs
		1071	A1179870			ESTs
9181 C,D						ESTs
9190 H		702	A1100835			EST
						EST, Weakly similar to PE2R_RAT 20-ALPHA-HYDROXYXYSTERIOD DEHYDROGENASE [R.norvegicus]
9191 A		681	A1072107			ESTs
9192 E		805	A1137345			ESTs
						Rat MHC class II RT1.B beta gene, encoding cell surface glycoprotein beta chain, Rat mRNA for MHC class II antigen RT1.B-1 beta-chain, Rattus norvegicus MHC class II antigen RT1.B beta chain mRNA, partial cds
9223 Q		1417	M36151			

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
9245	A	684	A1072278			ESTs
9267	Q	685	A1072384			ESTs, Moderately similar to human formiminotransferase cyclodeaminase [H.sapiens]
9326	A	799	A1136514			ESTs, Moderately similar to SPIN [H.sapiens]
9331	A,C,D	689	A1072633			ESTs
9336	A	691	A1072643			ESTs
9372	S	692	A1072712			ESTs
9373	S	802	A1136714			ESTs
9374	R	854	A1169557			ESTs, Highly similar to CDN6 MOUSE CYCLIN-DEPENDENT KINASE 6 INHIBITOR [M.musculus]
9399	A	693	A1072812			ESTs
9402	O,R	101	AA819383			ESTs
9423	S	1556	NM_012649		Ryudocan/syndecan 4	Ryudocan/syndecan 4
9424	N	1556	NM_012649		Ryudocan/syndecan 4	Ryudocan/syndecan 4
9425	A	27	AA800059		Ryudocan/syndecan 4	Ryudocan/syndecan 4
9432	E	695	A1072914			EST
9475	A,O	698	A1073059			ESTs
9486	L	69	AA818490			ESTs
9541	A	1704	NM_022542		Rat rhoB gene mRNA, complete cds	Rat rhoB gene mRNA, complete cds
9572	R	660	A1071162			ESTs
9583	A	664	A1071185			ESTs
9595	B,E,Q	800	A1136630			ESTs
9598	E	1365	H33832			ESTs
9603	E	666	A1071227			ESTs
9621	O	937	A1175486		ribosomal protein S7	Rat PRRHS8 mRNA for ribosomal protein S8

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GLCC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
9627	A		840	AI169041		ESTs
9635	N		676	AI071967		ESTs, Weakly similar to Y281, HUMAN
9668	K		669	AI071538		HYPOTHETICAL PROTEIN KIA0281 [H.sapiens]
9674	L		1044	AI178784		ESTs
9697	K		671	AI071642		ESTs
						EST
9712	B,E		988	AI176836		ESTs, Weakly similar to F25H5.6 [C.elegans]
9754	A		768	AI112194		ESTs
9766	R		672	AI071858		ESTs
9775	L		124	AA849767		Rattus norvegicus brain-enriched SH3-domain protein mRNA, complete cds
9784	C		710	AI101226		ESTs
9796	C		677	AI071990		Rattus norvegicus pEachy mRNA, complete cds
						ESTs, Weakly similar to AF165892_1 RNA-binding protein SlahBP [R.norvegicus]
9800	R		678	AI072014		ESTs
9826	A,M		228	AA891950		EST
						ESTs
9889	A		618	AI044621		ESTs
9905	A,G		221	AA891774		ESTs
9925	S		620	AI044925		ESTs
9969	K		622	AI045195		EST
9977	M		623	AI045253		EST
						ESTs, Highly similar to myosin X [M.musculus]
10002	K		816	AI137988		Actin-related protein complex 1b
10016	F,I		1673	NM_019289		ESTs
10019	J		1043	AI178756		

TABLE 1					Document Number 1650775	
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
10093 G		639	AI058746			EST
10109 A		1502	X58465		Ribosomal protein S5	Ribosomal protein S5
10176 A		102	AA819530			Rattus norvegicus E-sepin long form mRNA, complete cds
10184 E		1363	H33426			ESTs
10187 E		985	AI176781			ESTs
10200 L		644	AI059444			ESTs
10248 A		1574	NM_012797		Inhibitor of DNA binding 1, helix-loop-helix protein (splice variation)	Inhibitor of DNA binding 1, helix-loop-helix protein (splice variation)
10306 I		506	AF100470			Rattus norvegicus SERP1 mRNA, complete cds
10378 F		1205	AI233300		Complement component 5	ESTs, Moderately similar to CO5 HUMAN COMPLEMENT C5 PRECURSOR [H sapiens]
10394 R		337	AA943564			ESTs
10509 A		1696	NM_022268	Starch and sucrose metabolism	HLs:phosphorylase, glycogen; liver (Hers disease, glycogen storage disease type VI)	R norvegicus gene for glycogen phosphorylase (liver type) ESTs, Highly similar to HG17 RAT NONHISTONE CHROMOSOMAL PROTEIN HMG-17 [R.norvegicus]
10533 S		635	AI058430			EST
10540 O		269	AA894027			Rattus norvegicus outer mitochondrial membrane receptor rTOM20 mRNA, complete cds
10544 A,B		1341	D63411			Rattus norvegicus outer mitochondrial membrane receptor rTOM20 mRNA, complete cds
10545 A		1455	U21871			Rattus norvegicus outer mitochondrial membrane receptor rTOM20 mRNA, complete cds
10549 C,D,E		39	AA801255			ESTs

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TABLE 1

GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
10593	R	876	AI170673			ESTs
10594	E	704	AI100878			ESTs, Highly similar to EST00098 protein [H.sapiens]
10611	O	1018	AI177790			ESTs
10667	N	1273	AI236366			Rattus norvegicus RNA-binding protein
10790	F.M	602	AI043728			SiahBP mRNA, partial cds
10879	A.N	687	AI072476			EST
10984	A.P	842	AI169156			ESTs
11021	A.N	106	AA819767			ESTs, Weakly similar to HP33 [R.norvegicus]
11039	G	1705	NM_022543			ESTs
11048	E	668	AI071456			Rattus norvegicus steroid sensitive gene 1 protein (SSG-1) mRNA, complete cds
11125	L	673	AI071867			EST, Moderately similar to AF099186_1 EH domain-containing protein EHD1 [M.musculus]
11127	E	674	AI071868			ESTs, Highly similar to phosphatidylserine synthase-2 [M.musculus]
11152	G	1629	NM_017073	Aminoacyl-tRNA biosynthesis, Arginine and proline metabolism, Glutamate metabolism, Nitrogen metabolism, Porphyrin and chlorophyll metabolism	Glutamine synthetase (glutamate-ammonia ligase)	Glutamine synthetase (glutamate-ammonia ligase)

TABLE 1				Document Number: 1650775		
GLCC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
				Aminoacyl-tRNA biosynthesis, Arginine and proline metabolism, Glutamate metabolism, Nitrogen metabolism, Porphyrin and chlorophyll metabolism	Glutamine synthetase (glutamate-ammonia ligase)	Glutamine synthetase (glutamate-ammonia ligase)
11153 G		1629 NM_017073				ESTs
11157 A,E		1184 AF232494				ESTs, Highly similar to KIAA0315 [H.sapiens]
11166 A		40 AA801346				ESTs, Weakly similar to TISB_RAT TIS11B PROTEIN [R.norvegicus]
11172 P		338 AA943730				ESTs
11174 E		333 AA942745				ESTs
11179 A,H		783 AI111559				ESTs
11205 A,G		919 AI172057				ESTs, Moderately similar to weak similarity to Arabidopsis thaliana ubiquitin-like protein 8 [C.elegans]
11215 E		49 AA817921				ESTs
11227 O		541 AI010660				ESTs
11228 A		739 AI102871				ESTs, Weakly similar to similar to C.elegans hypothetical protein CET01H8.1,CEC05C12.3,CEF54D1.5, similar to trp and trp-like proteins [H.sapiens]
11235 D		1068 AI179709				ESTs, Moderately similar to hepatoma-derived growth factor [M.musculus]
11280 R		808 AI137420				ESTs, Moderately similar to imogen 44 [M.musculus]
11315 R		892 AI171229				

TABLE 1				Document Number: 1650775		
GLCC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
11322 E		526	AI009492			ESTs, Highly similar to Unknown [H.sapiens]
11331 C		828	AI145556			ESTs
11336 R		388	AA946441			ESTs
11354 R		833	AI146215			ESTs
11357 A		835	AI146237			ESTs
				Arginine and proline metabolism, Selenoamino acid metabolism, Urea cycle and metabolism of amino groups, beta-Alanine metabolism		
11403 A,D,L		889	AI171088	Arginine and proline metabolism, Selenoamino acid metabolism, Urea cycle and metabolism of amino groups, beta-Alanine metabolism	Hm:m.spermidine synthase	ESTs, Highly similar to SPEE_MOUSE SPERMIDINE SYNTHASE [M.musculus]
11404 A,C,D,L		1291	AI237002	Arginine and proline metabolism, Selenoamino acid metabolism, Urea cycle and metabolism of amino groups, beta-Alanine metabolism	Hm:m.spermidine synthase	ESTs, Highly similar to SPEE_MOUSE SPERMIDINE SYNTHASE [M.musculus] ESTs, Moderately similar to PTN3_HUMAN PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 3 [H.sapiens]
11422 Q		26	AA799812			ESTs, Moderately similar to PTN3_HUMAN PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 3 [H.sapiens]
11423 B,H,Q		26	AA799812			

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
						ESTs, Moderately similar to PTN3, HUMAN PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 3 [H.sapiens]
11426 H		896	AI171305			ESTs
11429 A G		862	AI169706			ESTs
11438 E		922	AI172189			ESTs
						ESTs, Moderately similar to 41BB, MOUSE 4-1BB LIGAND RECEPTOR PRECURSOR [M.musculus]
11465 O		1263	AI236084			ESTs, Moderately similar to progression elevated gene 3 protein [R.norvegicus] Rattus norvegicus progression elevated gene 3 protein mRNA, complete cds
11483 J		487	AF020618			ESTs, Highly similar to nuclear transcriptional repressor Mph1 [M.musculus]
						ESTs
11485 E		1248	AI235348			ESTs, Weakly similar to putative serine/threonine protein kinase MAK-V [M.musculus]
11492 A		770	AI105145			ESTs
11493 J		1356	H31287			ESTs, Weakly similar to putative serine/threonine protein kinase MAK-V [M.musculus]
11494 J		1356	H31287			ESTs, Weakly similar to putative serine/threonine protein kinase MAK-V [M.musculus]
11495 J		991	AI176901			ESTs, Weakly similar to putative serine/threonine protein kinase MAK-V [M.musculus]
11504 A B		906	AI171652			ESTs

TABLE 1					Document Number 1650775	
GLC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
11693	A,C,D,E,K	836	AI168953			Rattus norvegicus mRNA for Sulfotransferase K2
11700	E	557	AI012574			ESTs
11720	B,O,Q	1174	AI232273			ESTs, Highly similar to RNA cyclase homolog [H.sapiens]
11724	K	736	AI02812			ESTs
11731	P	1544	NM_012561		Follistatin	
11742	A,E	713	AI101262			ESTs
11745	A	475	AB006450		translocator of inner mitochondrial membrane 17 kDa, a	translocator of inner mitochondrial membrane 17 kDa, a
11821	O	653	AI070350			ESTs, Weakly similar to DPT1_MOUSE
11830	N	1052	AI179093			POLYPOSIS LOCUS PROTEIN 1
						HOMOLOG [M.musculus]
11840	N	1526	Y15068			ESTs
						Rattus norvegicus mRNA for Hsp70/Hsp90 organizing protein
11850	G	1431	R46985			R norvegicus mRNA for ribosomal protein L10a
11876	L	522	AI009321			ESTs
11893	B	1139	AI230951			ESTs
					Brain immunoglobulin like protein with tyrosine - based activation motifs, Protein tyrosine phosphatase, non-receptor type substrate 1 (SHP substrate 1)	Brain immunoglobulin like protein with tyrosine - based activation motifs, Protein tyrosine phosphatase, non-receptor type substrate 1 (SHP substrate 1)
11904	B,F,M,Q	1344	D85183			ESTs
11940	F,H	209	AA891108			ESTs
11959	A	217	AA891735			ESTs

TABLE 1				Document Number: 1650775		
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
11960 K		220	AA891740			ESTs, Weakly similar to EPOR, RAT
11974 B		363	AA944958			ERYTHROPOIETIN RECEPTOR PRECURSOR [R.norvegicus]
						ESTs
12058 R		1393	L25387	Fructose and mannose metabolism;Galactose metabolism;Glycolysis / Gluconeogenesis;Pentose phosphate cycle	Hsp-6-PHOSPHOFRUCTOKINASE, TYPE C	ESTs, Highly similar to K6PP, RAT 6-PHOSPHOFRUCTOKINASE, TYPE C [R.norvegicus]
12064 A		32	AA800429			ESTs
12087 A		1683	NM_020082		ribonuclease 4	ribonuclease 4
12120 O		121	AA849365			ESTs
12155 K		1370	J00728	Fatty acid metabolism, Tryptophan metabolism	cytochrome P450, 2b19	cytochrome P450, 2b19
12156 B,G,K		1378	K00996	Fatty acid metabolism, Tryptophan metabolism	cytochrome P450, 2b19	cytochrome P450, 2b19
12157 K		1379	K01721	Fatty acid metabolism, Tryptophan metabolism	cytochrome P450, 2b19	cytochrome P450, 2b19
12158 K		1383	L00320	Fatty acid metabolism, Tryptophan metabolism	cytochrome P450, 2b19	cytochrome P450, 2b19
12160 A,K		66	AA818412	Fatty acid metabolism, Tryptophan metabolism	cytochrome P450, 2b19	cytochrome P450, 2b19
12185 E		890	AI171094			ESTs, Weakly similar to Cys2/His2 zinc finger protein [R.norvegicus]
12198 R		273	AA899195			Rattus norvegicus replication factor C subunit 2 (RFC2) mRNA, partial cds
12203 L		274	AA899256			ESTs, Weakly similar to translation initiation factor [M.musculus]

TABLE 1			Document Number 1650775		
GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Uligenie Cluster Title
12215 E.S	696	AI072959			ESTs, Moderately similar to monoglyceride lipase [M.musculus]
12216 A	1106	AI229240			ESTs
12277 M.P	342	AA943800			ESTs
12306 A.E.N	360	AA944898			ESTs
12312 A	263	AA893453			ESTs
12314 G	372	AA945596			ESTs, Moderately similar to LECT2 precursor [H.sapiens]
12317 E.R	1237	AI234361			ESTs
12331 A	389	AA946466			ESTs, Weakly similar to cytoplasmic aminopeptidase P [R.norvegicus]
12332 A	389	AA946466			ESTs, Weakly similar to cytoplasmic aminopeptidase P [R.norvegicus]
12361 O	433	AA965031			ESTs
12375 L	798	AI136478			ESTs, Highly similar to p116Rip [M.musculus]
12450 A.P	755	AI103955			ESTs, Weakly similar to predicted using Genefinder [C.elegans]
12463 Q	1191	AI232706			ESTs
12467 S	1193	AI232924			ESTs
12471 A	413	AA957433			ESTs
12551 I	1122	AI230056			ESTs
12577 F.M	779	AI111344			Rattus norvegicus cydlin H mRNA, complete cds
12585 O	380	AA946034			ESTs, Highly similar to AF151803.1 Cgl
12587 A	1120	AI229979			45 protein [H.sapiens]
12613 I	1357	H31620			ESTs, Highly similar to hypothetical protein [H.sapiens]

TABLE 1					Document Number 1650775	
GLCC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
12614	C,D,R	933	A1175294			ESTs
12625	R	458	AA98029			ESTs
12655	A,O	1226	A1233836			ESTs
12694	A	416	AA957906			ESTs
						ESTs, Weakly similar to LIS1_MOUSE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB ALPHA SUBUNIT [R.norvegicus]
12714	P	533	A1010050			ESTs
12746	O	548	A1011809			ESTs
12844	N	679	A1072054			ESTs
12848	A,G	251	AA892916			ESTs, Weakly similar to hemomucin [D.melanogaster]
12857	N	694	A1072866			ESTs
12880	E	782	A1111558			ESTs
12928	B,F,R	396	AA955564			ESTs
12946	A,N	1088	A1228291			ESTs
12956	L	1296	A1237580			ESTs
12964	N	1267	A1236227			ESTs
12965	C	792	A1112926			ESTs
12969	J	794	A1112969			ESTs
					IHs: UDP-N-acetylglucosamine pyrophosphorylase 1	ESTs
12999	C	956	A1176276	Aminosugars metabolism		ESTs
13045	M	801	A1136702			ESTs
13055	E	1054	A1179100			ESTs, Highly similar to potential membrane protein C14orf1 [H.sapiens]
						ESTs, Highly similar to CBG_RAT CORTICOSTEROID-BINDING GLOBULIN PRECURSOR [R.norvegicus]
13088	A,F,G	266	AA893495			

TABLE 1					Document Number 1650775	
GLC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
13092 O		1158	A1231547		HMm:FK506 binding protein 4 (59 kDa)	ESTs, Weakly similar to PPP5 _{RAT} SERINE/THREONINE PROTEIN PHOSPHATASE 5 [R.norvegicus]
13093 B.O		552	A1012177			ESTs, Weakly similar to PPP5 _{RAT} SERINE/THREONINE PROTEIN PHOSPHATASE 5 [R.norvegicus]
13166 A.R		1039	A1178736			ESTs, Weakly similar to PPP5 _{RAT} SERINE/THREONINE PROTEIN PHOSPHATASE 5 [R.norvegicus]
13175 E		965	A1176465			ESTs
13203 A.C		1096	A1228728			ESTs
13229 O		154	AA658760		HMm:FK506 binding protein 4 (59 kDa)	ESTs
13251 C.D.R		1059	A1179264			ESTs
13265 J		719	A1101708			ESTs
13283 A		1598	NM_013078	Arginine and proline metabolism, Urea cycle and metabolism of amino groups	Ornithine carbamoyltransferase	Ornithine carbamoyltransferase
13294 D		1220	A1233731			ESTs, Weakly similar to TCPA _{RAT} T-COMPLEX PROTEIN 1, ALPHA SUBUNIT [R.norvegicus]
13332 B.Q		257	AA693080			ESTs
13351 A.H		62	AA618271			ESTs
13353 M.N		938	A1175508			ESTs
13458 C.D.I		934	A1175338			ESTs
13467 C		817	A1138034	Sphingoglycolipid metabolism	HHs:UDP-glucose ceramide glucosyltransferase	Ratius norvegicus UDP-glucose:ceramide glucosyltransferase mRNA, complete cds
13501 R		957	A1176284			ESTs
13534 E		382	AA946187			ESTs

TABLE 1					Document Number: 1650775	
GLCC Comparison ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
13557	B,E,L,N	367	AA945090			ESTs
13568	H	28	AA800169			ESTs
13580	K	1030	AI178507			ESTs
13581	E	1035	AI178602			ESTs
						ESTs, Highly similar to S/6612 transcription factor ATF-4 - mouse [M.musculus]
13634	A	1061	AI179381			ESTs
13640	E,H	814	AI137781			ESTs, Highly similar to RL3_RAT 60S RIBOSOMAL PROTEIN L3 [R.norvegicus]
13646	C,D,E	1509	X62166			Rattus norvegicus serine protease gene, complete cds
13684	A,D,I	81	AA818770			ESTs, Rat alpha-crystallin B chain mRNA, complete cds
13723	D	1419	M55534		Crystallin, alpha polypeptide 2	ESTs
13749	A	1089	AI228540			ESTs
13757	A	1094	AI228676			ESTs
13762	A,E	1129	AI230326			ESTs
13799	L	947	AI175871			ESTs
13812	R	1101	AI229167			ESTs
13838	R	1111	AI229416			ESTs
13874	C,D	1117	AI229832			ESTs, Weakly similar to KIAA0859 protein [H.sapiens]
13895	M	1127	AI230270			ESTs
13918	E	569	AI013832			ESTs
13925	H	17	AA799601			ESTs
13932	E,H,N	1142	AI230988			ESTs

TABLE 1					Document Number 1650775	
GLCC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
13949	R	1149	A1231193			ESTs, Moderately similar to SEC_HUMAN SEC PROTEIN [H.sapiens]
13963	A.O	1154	A1231388			ESTs
13967	E	1155	A1231439			EST
13992	Q	1281	A1236679			ESTs
14007	A.E	1166	A1231808			ESTs
14016	F	489	AF026505			Rattus norvegicus SH3-containing protein p4015 mRNA, complete cds
14017	F	211	AA891194			Rattus norvegicus SH3-containing protein p4015 mRNA, complete cds
14035	A	1177	A1232328	Tyrosine metabolism	HHs:homogentisate 1,2-dioxygenase (homogentisate oxidase)	ESTs, Highly similar to homogentisate 1,2-dioxygenase [M.musculus]
14051	A.C.D	1183	A1232489			ESTs, Weakly similar to PIR1 [H.sapiens]
14053	E	1243	A1235046			ESTs, Highly similar to DDX6 MOUSE PROBABLE ATP-DEPENDENT RNA HELICASE P54 [M.musculus]
14074	A	1206	A1233323			ESTs
14081	P	1198	A1233164			ESTs
14083	A	1009	A1177181			ESTs
14095	A	1211	A1233468			ESTs
14103	A	1199	A1233172			ESTs, Weakly similar to AF073727_1 EH domain-binding mitotic phosphoprotein [H.sapiens]
14116	S	1207	A1233361			ESTs
14118	A	1208	A1233367			EST

TABLE 1					Document Number: 1650775	
GLC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
14126 E		1062	AI179415		His:neurotrophic tyrosine kinase, receptor, type 1	Rattus norvegicus tropomyosin non-muscle isoform NM1 (TPM-gamma) mRNA, complete cds. Rattus norvegicus tropomyosin non-muscle isoform NM3 (TPM-gamma) mRNA, complete cds
14139 H		175	AA859700	Porphyryn and chlorophyll metabolism		EST, Highly similar to PPOX_MOUSE PROTOPORPHYRINOGEN OXIDASE [M.musculus], EST, Moderately similar to PPOX_HUMAN PROTOPORPHYRINOGEN OXIDASE [H.sapiens] ESTs, Weakly similar to cDNA EST yk249b3.5 comes from this gene [C.elegans] ESTs ESTs Rattus norvegicus guanine aminohydrolase (GAH) mRNA, complete cds
14171 E		1024	AI178073			
14181 A		1233	AI234107			
14185 P		177	AA859837	Purine metabolism	Hmm:guanine deaminase	
14195 E		775	AI105205			ESTs
14199 K		1234	AI234133			ESTs
14206 A		182	AA859994			ESTs
14208 A,B		723	AI102017			ESTs
14224 C		1140	AI230956			ESTs, Moderately similar to TF-G protein [M.musculus]
14242 C,D		1086	AI228197			ESTs
14250 K		21	AA799729	Purine metabolism	Phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4)	ESTs, Phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E4)

TABLE 1					Document Number: 1650775	
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
14258	C	1118	AI229902			ESTs
14264	S	1181	AI232409			ESTs, Weakly similar to bk126B4.2 [H.sapiens]
14266	O	1366	H33842			ESTs, Highly similar to phosphoprotein [M.musculus]
14303	L	1148	AI231159			ESTs, Highly similar to KIAA1049 protein [H.sapiens]
14312	A,E	1261	AI236036			ESTs, Moderately similar to UBE-1b [M.musculus]
14330	P	233	AA892146			ESTs
14335	E	1006	AI177115			ESTs
14353	A	171	AA859585			ESTs
14400	F,M	858	AI169620			ESTs
14424	A,J	654	AI070421			ESTs
14449	E	1235	AI234152			ESTs
14458	C,I	826	AI145095			ESTs
14462	C,D	703	AI100871			ESTs
14485	F	253	AA892950			ESTs, Moderately similar to mitochondrial DNA polymerase accessory subunit [M.musculus]
14491	M	535	AI010147			ESTs
14504	M,P	25	AA799804			ESTs
14506	A	1359	H32584			ESTs
14507	S	132	AA850618			ESTs, Highly similar to gp250 precursor [M.musculus]
14512	A,G	793	AI112964			ESTs
14584	A	1250	AI235360			ESTs, Moderately similar to glutathione-S-transferase homolog [M.musculus]

TABLE 1					Document Number 1650775	
GLQC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
14595 S		232	AA892128			ESTs
14600 E,R		38	AA801076			ESTs
14619 C,D		1290	AI236989			ESTs
14638 E		803	AI137049			ESTs, Moderately similar to Nlbrin [M.musculus]
14693 A,C,D		1240	AI234830			ESTs, Weakly similar to ORF YKR081c [S.cerevisiae]
14738 N,O		997	AI176993			ESTs
14746 A		1252	AI235584			ESTs, Moderately similar to KIAA0922 protein [H.sapiens]
14767 A		1256	AI235895			ESTs
14776 A,E,N		1258	AI235950			ESTs
14840 K		1301	AI237698			ESTs, Weakly similar to /prediction
14869 A		1264	AI236089			ESTs, Weakly similar to /prediction
14882 S		1324	D00362		Esterase 2	Esterase 2
14913 L,R		1274	AI236461			ESTs
14937 A,E		1293	AI237159			ESTs, Highly similar to lipic acid synthetase [H.sapiens]
14939 C,D		1090	AI228557			ESTs
14958 N		105	AA819744			ESTs
14959 I		1444	U03390			Rattus norvegicus Sprague Dawley protein kinase C receptor mRNA, complete cds
						ESTs, Highly similar to integrase interactor 1a protein [M.musculus], Rattus norvegicus Sprague Dawley protein kinase C receptor mRNA, complete cds
14960 A,G,O		897	AI171319			

TABLE 1				Document Number 1650775		
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
15055 A		1463	U48220	Fatty acid metabolism, Tryptophan metabolism	Hhs:cytochrome P450, subfamily IID (debrisoquine, sparteine, etc., - metabolizing), polypeptide 6	Rattus norvegicus cytochrome P450 2D18 mRNA, complete cds
15057 O		1675	NM_019291	Nitrogen metabolism	carbonic anhydrase 2	carbonic anhydrase 2
15070 H		1081	AI180442	Sterol biosynthesis	Hhs:farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase)	Rat testis-specific farnesyl pyrophosphate synthetase mRNA, complete cds
15080 A		724	AI102045			ESTs, Highly similar to OS-4 protein [H.sapiens]
15089 F		530	AI009752			ESTs
15091 J		1040	AI178740			ESTs
15097 LO		1548	NM_012588		YY1 transcription factor	ESTs
15113 AG		941	AI175590		Insulin-like growth factor-binding protein (IGF-BP3)	Insulin-like growth factor-binding protein (IGF-BP3)
15116 P		190	AA874928			ESTs, Highly similar to dJ1118D24.1c [H.sapiens]
15121 E		746	AI103159			ESTs, Highly similar to sorting nexin 4 [H.sapiens]
15122 E		1176	AI232303			Rattus norvegicus interferon-inducible protein 16 mRNA, complete cds
				Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism		ESTs, Weakly similar to Sid1669p [M.musculus]
15127 BK		1434	S56937		UDP-glucuronosyltransferase 1 family, member 1	Rattus norvegicus UDP-glucuronosyltransferase (UGT1.1) gene, complete cds, Rattus norvegicus UDP-glucuronosyltransferase UGT1A7 mRNA, complete cds, UDP-glucuronosyltransferase 1 family, member 1

TABLE 1				Document Number 1650775		
GLCC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
15135	A.D	1436	S71021			R.norvegicus mRNA for ribosomal protein L6
15136	A	20	AA799672			R.norvegicus mRNA for ribosomal protein L6
15139	H	818	A1144585			ESTs
15141	E.F	1649	NM_017278		proteasome (prosome, macropain) subunit, alpha type 1	proteasome (prosome, macropain) subunit, alpha type 1
15149	R	164	AA859327			ESTs
15166	A.E	165	AA859341			ESTs, Highly similar to KIAA0418
15162	L	168	AA859350			[H.sapiens]
15170	A.H.N	1299	A1237618			ESTs
15171	J	1160	A1231792			ESTs, Moderately similar to BAG-family molecular chaperone regulator-3
15172	J	169	AA859362			[H.sapiens]
15179	R	982	A1176675			ESTs, Moderately similar to BAG-family molecular chaperone regulator-3
15181	H	1245	A1235234			[H.sapiens]
15189	M.N	1399	M11794			ESTs
15190	N	729	A1102562		Metallothionein	Metallothionein
15191	N	964	A1176456		Metallothionein	Metallothionein
15197	A	778	A1105444			ESTs
15203	I	1389	L19698			Rat GTP-binding protein (rat A) mRNA, complete cds
15207	A.B.Q	147	AA858448			ESTs
15239	A	1619	NM_016989			R.norvegicus (Sprague Dawley) ribosomal protein L15 mRNA

TABLE 1

TABLE 1				Document Number 165077		
GLCC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
15240_A		609	A1044241			ESTs, Moderately similar to cell death activator CIDE-B [M.musculus]
15251_E.L		1011	A1177363			ESTs, Highly similar to CSK_RAT TYROSINE-PROTEIN KINASE CSK [R.norvegicus]
15281_I		1328	D13623			ESTs
15282_D.I.L		1034	A1178573			ESTs
15283_D		148	AA858548			ESTs
15291_J		780	A1111401		multiple inositol polyphosphate histidine phosphatase 1	multiple inositol polyphosphate histidine phosphatase 1
15292_J		484	AF012714		multiple inositol polyphosphate histidine phosphatase 1	multiple inositol polyphosphate histidine phosphatase 1
15295_O		1602	NM_013102		FK506-binding protein 1 (12kD)	FK506-binding protein 1 (12kD)
15299_A		1647	NM_017259		B-cell translocation gene 2, anti-proliferative	B-cell translocation gene 2, anti-proliferative
15300_A.F		1647	NM_017259		B-cell translocation gene 2, anti-proliferative	B-cell translocation gene 2, anti-proliferative
15301_A		1647	NM_017259		B-cell translocation gene 2, anti-proliferative	B-cell translocation gene 2, anti-proliferative
15312_C.D,I,J		198	AA875126			ESTs
15313_C.D,J		198	AA875126			ESTs
15315_G		1021	A1177911		calpactin I heavy chain	calpactin I heavy chain
15345_L		902	A1171587			ESTs
15365_D		1637	NM_017147		cofilin 1, non-muscle	cofilin 1, non-muscle
15374_C.D		1368	H34186			ESTs, Highly similar to IF39_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9 [H.sapiens]

TABLE 1					Document Number: 1650775	
GLC Comparison ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
15382	A,J	926	AI172302			ESTs, Weakly similar to S43056 hypothetical protein - mouse [M.musculus]
15391	K	534	AI010083			Rat mRNA for HBP23 (heme-binding protein 23 kDa), complete cds
15398	C	1277	AI236566			ESTs
15433	L	1641	NM_017187		high mobility group protein 2	high mobility group protein 2
15441	K	834	AI146216			EST
15462	G	1447	U06230			Rattus norvegicus protein S mRNA, partial cds
15467	H	1285	AI236106			ESTs
15480	F	201	AA875362			ESTs
15490	J	1107	AI229253			Rattus norvegicus zinc finger protein (pMLZ-4) mRNA, 3' untranslated region
15491	H	979	AI176542			ESTs
15500	K	1110	AI229337			ESTs
15503	P	1688	NM_019237		procollagen C-proteinase enhancer protein	procollagen C-proteinase enhancer protein
15504	M,P	1688	NM_019237		procollagen C-proteinase enhancer protein	procollagen C-proteinase enhancer protein
15519	A	1036	AI178629		Proteasome (prosome, macropain) subunit, beta type, 8 (low molecular mass polypeptide 7)	ESTs, Highly similar to PRCY_RAT PROTEASOME COMPONENT C-13 PRECURSOR [R.norvegicus]
15534	O	955	AI176266			ESTs
15535	F	1653	NM_017283		proteasome (prosome, macropain) subunit, alpha type 6	proteasome (prosome, macropain) subunit, alpha type 6
15543	D,I	1163	AI231800			ESTs

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
15551 R		1138	AI230759			ESTs, Moderately similar to ornithine decarboxylase antizyme 2 [M.musculus]
15558 J		204	AA875537			ESTs
15571 G		1413	M27207		procollagen, type I, alpha 1	R.norvegicus mRNA for collagen alpha1 type I
15606 B.N		356	AA944401			ESTs
15612 A		1618	NM_016987	Citrate cycle (TCA cycle)	ATP citrate lyase	ATP citrate lyase
15616 J		1562	NM_012699		Microvascular endothelial differentiation gene 1	Microvascular endothelial differentiation gene 1
15617 J		205	AA875620			ESTs
15634 H		1546	NM_012576		Glucocorticoid receptor	Glucocorticoid receptor
15642 A		1016	AI177503			R.norvegicus mRNA for histone H3.3
15645 K		879	AI170709			R.norvegicus mRNA for histone H3.3
15647 A,J		488	AF025424	Purine metabolism, Pyrimidine metabolism	HMm:RNA polymerase 1-2 (128 kDa subunit)	Rattus norvegicus RNA polymerase I 127 kDa subunit mRNA, complete cds
15655 I,L		733	AI102739			ESTs
15663 D,R		940	AI175566			Rattus norvegicus mRNA for Tclex-1, complete cds
15672 S		281	AA900009			Rat mRNA for 5E5 antigen, complete cds
15673 G		921	AI172107			Rat mRNA for 5E5 antigen, complete cds
15700 A,D		479	AB010466			Rattus norvegicus mRNA for multidrug resistance-associated protein (MRP)-like protein-1 (MLP-1), complete cds
15701 F,G		1645	NM_017220			Rattus norvegicus mRNA for multidrug resistance-associated protein (MRP)-like protein-2 (MLP-2), complete cds

TABLE 1					Document Number 1650775	
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
15755 A,K		1718	NM_022960			Rattus norvegicus neutral solute channel aquaporin 9 (AQP9) mRNA, complete cds
15778 E		1726	NM_024163			Rattus norvegicus brain-enriched guanylate kinase-associated protein 1 mRNA, complete cds
15786 B,Q		575	AI013924			ESTs
15834 B,E		286	AA900580	Oxidative phosphorylation, Ubiquinone biosynthesis	Hhs:NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 (14.5kD, B14.5b)	ESTs, Moderately similar to NADH-ubiquinone oxidoreductase B14.5B subunit [H.sapiens]
15860 D		738	AI102868			ESTs, Weakly similar to phosphoserine aminotransferase [H.sapiens]
15861 C,D		738	AI102868			ESTs, Weakly similar to phosphoserine aminotransferase [H.sapiens]
15862 A,C,D		1126	AI230228			ESTs, Weakly similar to phosphoserine aminotransferase [H.sapiens]
15884 A,Q		185	AA866276			ESTs
15888 K		199	AA875225			Rat guanine nucleotide-binding protein G i, alpha subunit mRNA, complete cds
15892 A,F		1074	AI179988			ESTs
15900 A,C,D		1202	AI233262			ESTs
15914 F		451	AA997711			ESTs
15933 A		200	AA875253			R.norvegicus ARL 1 mRNA for ARF-like protein 1
15955 A,K,L		1175	AI232294			ESTs

TABLE 1					Document Number 1650775	
GLCC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
15959	E.L	972	A1176540			ESTs
15961	P	550	A012130			ESTs
15980	H	186	AA866426			ESTs
15987	K	187	AA866435			EST
16006	A.F	497	AF062594			Rattus norvegicus nucleosome assembly protein mRNA, complete cds
16023	G	225	AA891872	Nicotinate and nicotinamide metabolism	Nicotinamide nucleotide transhydrogenase (NAD(P)+ transhydrogenase)	ESTs, Highly similar to NAD(P)+ transhydrogenase [M.musculus]
16053	L	1091	AL228596			ESTs, Weakly similar to weakly similar to gastrula zinc finger protein [C.elegans]
16080	A.J.Q	1547	NM_012580	Porphyrin and chlorophyll metabolism	Heme oxygenase	Heme oxygenase
16081	A.J.Q	1067	A1179610	Porphyrin and chlorophyll metabolism	Heme oxygenase	Heme oxygenase
16085	A.C.D	189	AA874889			ESTs
16087	L	1145	AL231011			ESTs
16124	K	994	A1176963			ESTs, Weakly similar to melanocyte-specific gene 1 protein [R.norvegicus]
16125	Q	503	AF090134			Rattus norvegicus lin-7-Ba mRNA, complete cds
16134	A.H	285	AA893485			Rattus norvegicus clone BB.1.4.1 unknown Glu-Pro dipeptide repeat protein mRNA, complete cds
16167	E	191	AA874941			ESTs, Moderately similar to adpophillin [H.sapiens]

TABLE 1					Document Number 1650775	
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
16169	E	598	AI030932			ESTs, Moderately similar to adipophilin [H.sapiens]
16172	A	1179	AI232341			ESTs, Weakly similar to C13B9.2 [C.elegans]
16173	M,P	408	AA957003			Rattus norvegicus intercellular calcium-binding protein (MRP8) mRNA, complete cds
						ESTs, Weakly similar to ECHM_RAT ENOYL-COA HYDRATASE, MITOCHONDRIAL PRECURSOR [R.norvegicus]
16190	A,S	757	AI104482			Rat mRNA for ribosomal protein S8
16205	L	1488	X06423			ESTs, Moderately similar to AF133910_1 ARL-6 interacting protein-3 [M.musculus]
16215	H	192	AA874999			Secreted acidic cysteine-rich glycoprotein (osteonecin)
16219	G	1557	NM_012656			ESTs, Moderately similar to DHB2_RAT ESTRADIOL 17 BETA-DEHYDROGENASE 2 [R.norvegicus]
		166	AA859342			Rat brain glucose-transporter protein mRNA, complete cds
16240	M					Solute carrier family 2 a 1 (facilitated glucose transporter) brain
16251	E,Q	347	AA944077			Fatty acid metabolism, Tryptophan metabolism
16278	E,K	1338	D38381			Hsp-CYTOCHROME P450 3A18
16283	O	1667	NM_019229			solute carrier family 12, member 4
16312	A	193	AA875032			ESTs
16314	A	167	AA859348			ESTs
16317	B	194	AA875041			ESTs, Moderately similar to AF123655_1 FEZ1 [H.sapiens]

TABLE 1						Document Number: 1650775	
GLCC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title	
16318 J		174	AA859648			ESTs, Weakly similar to DnaJ homolog 2 [R.norvegicus]	
16319 K		195	AA875047			ESTs, Highly similar to TCPZ_MOUSE T	
16321 C		1157	AI231506			COMPLEX PROTEIN 1, ZETA	
16323 S		184	AA866240			SUBUNIT [M.musculus]	
16324 A		722	AI102009			ESTs	
						EST	
						ESTs	
16327 A.O		196	AA875050			ESTs, Weakly similar to choline/ethanolamine kinase [R.norvegicus]	
16361 H		1442	U01344		Hsp:ARYLAMINE N-ACETYLTRANSFERASE 1	Rattus norvegicus clone A-2 arylamine N acetyltransferase mRNA, complete cds	
16364 A.H		235	AA892251			R.norvegicus mRNA for V1a arginine vasopressin receptor	
16366 P		250	AA892888			EST	
16367 P		250	AA892888			EST	
16408 F		145	AA852027			ESTs	
16409 S		145	AA852027			ESTs	
						ESTs, Highly similar to SMD2_HUMAN SMALL NUCLEAR RIBONUCLEOPROTEIN SM D2 [H.sapiens]	
16438 I		958	AI176294			ESTs	
16446 A		214	AA891423			farnesyl diphosphate farnesyl transferase 1	
16449 H		1669	NM_019238	Sterol biosynthesis		ESTs	
16458 B.Q		362	AA944956				

TABLE 1				Document Number: 1650775		
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
16477 Q		983	AI176701			Rat low molecular weight fatty acid binding protein mRNA, complete cds
16513 C		118	AA848782			ESTs, Moderately similar to hypothetical protein [M.musculus]
16518 D		973	AI176546			ESTs, Weakly similar to HS9B_RAT
16519 P		1539	NM_012532			HEAT SHOCK PROTEIN HSP 90-BETA
16524 H		1362	H33219	Porphyrin and chlorophyll metabolism	Ceruloplasmin (ferroxidase)	[R.norvegicus]
16562 E,N		904	AI171630			Ceruloplasmin (ferroxidase)
16566 H		1131	A1230395			ESTs
16610 I		1333	D28557			Rattus norvegicus p38 mitogen activated protein kinase mRNA, complete cds
16616 R		1230	A1234079			Rattus norvegicus mRNA for TIP120, complete cds
16618 C		837	AI168967			Rattus norvegicus muscle Y-box protein YB2 mRNA, complete cds
16623 E		1150	A1231196			ESTs
16649 I		1606	NM_013132		Annexin V	Annexin V
16650 I		1606	NM_013132		Annexin V	Annexin V
16654 I		1522	X98517			R.norvegicus mRNA for macrophage metalloelastase (MME)
16673 R		759	AI104608			ESTs
16680 A		436	AA965190			ESTs

TABLE 1						Document Number 1650775
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
16683	I	1596	NM_013052		Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide
16684	I,O	1596	NM_013052		Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide
16688	L	870	AI170327			ESTs
16700	A,E,S	517	AI008838			ESTs, Weakly similar to LONN_HUMAN MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H.sapiens]
16701	A	517	AI008838			ESTs, Weakly similar to LONN_HUMAN MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H.sapiens]
16703	A,C,O	1060	AI179300			ESTs, Weakly similar to LONN_HUMAN MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H.sapiens]
16704	S	4	AA686132			ESTs, Weakly similar to LONN_HUMAN MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H.sapiens]
16726	A	1427	M86235	Fructose and mannose metabolism	Hsp-KETOHEXOKINASE	Rat ketohexokinase mRNA, complete cds
16728	H	1020	AI177885			ESTs

TABLE 1					Document Number: 1650775	
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
16730	A,I	23	AA799766			ESTs, Moderately similar to JTV1_HUMAN JTV-1 PROTEIN [H.sapiens]
16747	L	336	AA943131			ESTs
16756	C,D	52	AA818089			ESTs, Highly similar to glycol-HRNA synthetase [H.sapiens]
16765	A	632	AI058319			ESTs
16766	A	682	AI072137			ESTs
				Butanoate metabolism, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Lysine degradation, Propanoate metabolism, Tryptophan metabolism, Valine, leucine and isoleucine degradation, beta-Alanine metabolism	HHs:hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	Rat mRNA for mitochondrial long-chain enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase alpha-subunit of mitochondrial trifunctional protein, complete cds
16768	N	1331	D16478			ESTs, Highly similar to glutathione transferase [R.norvegicus]
16780	E,K	1510	X62660			ESTs, Weakly similar to nonmuscle myosin heavy chain-A [R.norvegicus]
16783	L,O	553	AI012215			
18809	B,O,Q	1503	X58828		Hsp:PROTEIN-TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 2	Rat PTP-S mRNA for protein-tyrosine phosphatase
18825	J	245	AA892602			ESTs
18854	I	188	AA866454			Rat alpha-2(I) promoter
18859	A,C,N	1283	AI236753			ESTs

TABLE 1					Document Number 1650775	
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
16894	O	144	AA852018			ESTs, Moderately similar to AF097362_1 gamma-interferon inducible lysosomal thiol reductase [H.sapiens]
16944	S	320	AA925541			ESTs, Highly similar to protein L [M.musculus]
16945	S	320	AA925541			ESTs, Highly similar to protein L [M.musculus]
				Arginine and proline metabolism, Glycine, serine and threonine metabolism, Urea cycle and metabolism of amino groups	Guanidinoacetate methyltransferase	Guanidinoacetate methyltransferase
16947	E	1572	NM_012793			EST
16958	G	92	AA819021			ESTs
16961	P	1058	AI179236		Insulin-like growth factor binding protein 1	Insulin-like growth factor binding protein 1
16982	A	1608	NM_013144			ESTs
16993	A	14	AA799560	Galactose metabolism, Nucleotide sugars metabolism, Pentose and glucuronate interconversions, Starch and sucrose metabolism		ESTs, Highly similar to UDP1_HUMAN UTP-GLUCOSE-1-PHOSPHATE URIDYLTRANSFERASE 1 [H.sapiens]
17027	A,E	877	AI170679		IHs: UDP-glucose pyrophosphorylase 2	ESTs, Weakly similar to Similarity to B. subtilis YQJC protein [C.elegans]
17049	A	929	AI172417			carboxyl reductase
17064	I	1660	NM_019170	Prostaglandin and leukotriene metabolism		

TABLE 1				Document Number: 1650775		
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
17090	G,K	1474	U73174	Glutamate metabolism, Glutathione metabolism	HHs:glutathione reductase	Rattus norvegicus glutathione reductase mRNA, complete cds
17091	G,K	1474	U73174	Glutamate metabolism, Glutathione metabolism	HHs:glutathione reductase	Rattus norvegicus glutathione reductase mRNA, complete cds
17092	K	259	AA893189	Glutamate metabolism, Glutathione metabolism	HHs:glutathione reductase	Rattus norvegicus glutathione reductase mRNA, complete cds
17107	E	1638	NM_017160		ribosomal protein S6	ribosomal protein S6
17117	K	1085	A1228042			ESTs, Weakly similar to AC007080_2 NG38 [M.musculus]
17154	A	1407	M15883			Rat clathrin light chain (LCB2) mRNA, complete cds; Rat clathrin light chain (LCB3) mRNA, complete cds
17157	I	326	AA926129			ESTs, Highly similar to AF168795_1 schlafen-4 [R.norvegicus]
17158	H	1699	NM_022298			Rat mRNA encoding alpha-tubulin
17167	M	566	A1013690			ESTs
17175	A	1501	X58389			R.norvegicus ASI mRNA for mammalian equivalent of bacterial large ribosomal subunit protein L22
17225	A,I	215	AA891553			ESTs, Highly similar to elf3 p66 [M.musculus]
17256	A	219	AA891739			ESTs, Weakly similar to p60 protein [R.norvegicus]
17257	E,R	1568	NM_012766		Cyclin D3	Cyclin D3
17258	P	1568	NM_012766		Cyclin D3	Cyclin D3
17261	R	1568	NM_012766		Cyclin D3	Cyclin D3
17277	B,P,Q	523	A1009338			Rattus norvegicus glycine-, glutamate-, thienylcydohexypiperidine-binding protein mRNA, complete cds

TABLE 1					Document Number 1650775	
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
17281	M,P	1450	U10697		Hsp LIVER CARBOXYLESTERASE 4 PRECURSOR	R. norvegicus mRNA for pl esterase (ES-4)
17291	E	931	A1172491	Citrate cycle (TCA cycle), Glutathione metabolism	Hh: isocitrate dehydrogenase 2 (NADP+), mitochondrial	ESTs, Weakly similar to IDHC. RAT ISOCITRATE DEHYDROGENASE [R. norvegicus]
17324	A	1686	NM_021593			Rattus norvegicus kynurenine 3- hydroxylase mRNA, complete cds
17334	A	151	AA858704			ESTs, Highly similar to responsible for hereditary multiple exotosis [M. musculus]
17335	A	732	A1102634			ESTs, Weakly similar to W0684.2 [C. elegans]
17337	J	472	AB000717	Methionine metabolism, Selenoamino acid metabolism	Hh: methionine adenosyltransferase II, alpha	ESTs
17339	A	123	AA849497			ESTs
17340	A,E	507	A1007803			Rattus norvegicus ERM-binding phosphoprotein mRNA, complete cds
17368	E,R	284	AA900548			ESTs
17369	C,I,P	812	A1137572			ESTs
17377	A	1491	X13058		Tumor protein p53 (Li-Fraumeni syndrome)	Rat mRNA for nuclear oncoprotein p53
17393	A,O	1377	J04943		Nucleoplasmin-related protein (Nuclear protein B23)	Nucleoplasmin-related protein (Nuclear protein B23)
17400	E	744	A1103097			ESTs, Highly similar to ATPK_MOUSE ATP SYNTHASE F CHAIN, MITOCHONDRIAL [M. musculus]
17401	A	1595	NM_013043		Transforming growth factor beta stimulated clone 22	Transforming growth factor beta stimulated clone 22

TABLE 1				Document Number 1660775		
GLCC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
						ESTs, Highly similar to DHYS_HUMAN DEOXYHYPPUSINE SYNTHASE [H.sapiens]
17451 E		806	AI137356			ESTs
17479 R		827	AI145385			R.norvegicus mRNA for RT1.Ma
17481 E		1529	Z49761			ESTs
17496 A		325	AA926109			Rattus norvegicus sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds
17500 I,P		1713	NM_022866			ESTs
17506 L		649	AI070068			
17516 O		1739	NM_017321		iron-responsive element-binding protein	iron-responsive element-binding protein
17524 A		539	AI010568		Epoxide hydrolase 1 (microsomal xenobiotic hydrolase)	Epoxide hydrolase 1 (microsomal xenobiotic hydrolase)
17541 G,K		1580	NM_012844			Rattus norvegicus mRNA for hnRNP protein, partial
17571 H,I		1276	AI236484			Rattus norvegicus mRNA for hnRNP protein, partial
17572 E		71	AA818524			ESTs
17589 A		248	AA892851			ESTs
17590 F		248	AA892851			ESTs
17591 A		898	AI171354			ESTs
17613 O		10	AA799511			ESTs
						ESTs, Weakly similar to FKBP1_RAT FK506-BINDING PROTEIN [R.norvegicus]
17617 E		1269	AI236301			ESTs
17644 R		293	AA924036			
17664 B,Q		1238	AI234496			ESTs

TABLE 1			Document Number: 1650775			
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
17672 N		1123	AI230074	Oxidative phosphorylation, Ubiquinone biosynthesis	Hm:NADH ubiquinone oxidoreductase subunit MWFE	ESTs, Highly similar to NIMM_MOUSE NADH-UBIQUINONE OXIDOREDUCTASE MWFE SUBUNIT [M.musculus]
17677 E		683	AI072246			
17683 N		700	AI073257			
17684 G		236	AA892345			ESTs
17685 K		797	AI113055			Rat mRNA for dimethylglycine dehydrogenase (EC number 1.5.99.2)
17687 C		12	AA799531			EST
17688 A		12	AA799531			ESTs, Weakly similar to predicted using Genefinder [C.elegans]
17695 N		1192	AI232784			ESTs, Weakly similar to predicted using Genefinder [C.elegans]
17699 O		135	AA851233			ESTs, Weakly similar to putative peroxisomal 2,4-dienoyl-CoA reductase [R.norvegicus]
17709 A		1456	U24489			ESTs, Weakly similar to NG28 [M.musculus]
17730 G		1709	NM_022697		Tenascin X	
17734 C,D		466	AA998683		Rat mRNA for ribosomal protein L28	
17735 C,D,J		981	AI176658		ESTs,Rattus norvegicus heat shock protein 27 (hsp 27) gene, complete cds	
17736 C,D		1428	M86389		ESTs,Rattus norvegicus heat shock protein 27 (hsp 27) gene, complete cds	
17747 E		1236	AI234223		ESTs,Rattus norvegicus heat shock protein 27 (hsp 27) gene, complete cds	
						ESTs, Highly similar to cellular apoptosis susceptibility protein [H.sapiens]

TABLE 1					Document Number 1650775	
GLSC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
17812 A,E		841	A1169075	Glutathione metabolism, Tyrosine metabolism	HMM:glutathione transferase zeta 1 (maleylacetate isomerase)	ESTs
17819 A		891	A1171095			ESTs, Highly similar to unknown [H.sapiens]
17844 A,E		398	AA956927			ESTs
17847 A		1025	A1178214			ESTs
17850 A		734	A1102750			ESTs, Weakly similar to TCGA, RAT T-COMPLEX PROTEIN 1, ALPHA SUBUNIT [R.norvegicus]
17854 Q		1490	X13016			Rat mRNA for MRC OX-45 surface antigen
17894 E,F		1594	NM_013027		Selenoprotein W muscle 1	Selenoprotein W muscle 1
17908 A,J		1670	NM_019242		interferon-related developmental regulator 1	interferon-related developmental regulator 1
17935 S		289	AA901006			Rattus norvegicus membrane interacting protein of RGS16 (Mir16) mRNA, complete cds
17950 Q		1278	A1236590		myeloid differentiation primary response gene 88	ESTs
17955 L		590	A1030069		adaptor-related protein complex AP-1, beta 1 subunit	ESTs
17956 I		427	AA964379			beta 1 subunit
17982 A		1727	NM_017010		Glutamate receptor, ionotropic, N-methyl D-aspartate 1	Glutamate receptor, ionotropic, N-methyl D-aspartate 1, Rat N-methyl-D-aspartate receptor (NMDAR1) gene, first exon

TABLE 1					Document Number:1650775	
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc.ID	Pathways	Known Gene Name	UniGene Cluster Title
18001 A		149	AA858573			ESTs, Highly similar to SP24_RAT SECRETED PHOSPHOPROTEIN 24 [R.norvegicus],Rattus norvegicus spp-24 precursor mRNA, partial cds
18002 A,D,E		600	A1043655			ESTs, Highly similar to SP24_RAT SECRETED PHOSPHOPROTEIN 24 [R.norvegicus],Rattus norvegicus spp-24 precursor mRNA, partial cds
18028 G		1337	D38062			Rattus norvegicus UDP-glucuronosyltransferase UGT1A7 mRNA, complete cds
18029 S		1418	M38759		Sex hormone binding globulin or androgen-binding protein	Sex hormone binding globulin or androgen-binding protein
18043 J		487	AF020618			Rattus norvegicus progression elevated gene 3 protein mRNA, complete cds
18046 I		500	AF072892			Rattus norvegicus versican V0 isoform mRNA, partial cds,Rattus norvegicus versican V3 isoform precursor, mRNA, complete cds
18082 S		478	AB010429			R.norvegicus mRNA for mitochondrial very-long-chain acyl-CoA thioesterase
18083 S		1524	Y09333		Hsp.ACYL COENZYME A THIOESTER HYDROLASE, MITOCHONDRIAL PRECURSOR	R.norvegicus mRNA for mitochondrial very-long-chain acyl-CoA thioesterase
18099 G		1604	NM_013119			ESTs, Highly similar to A60054 sodium channel protein IIb, long form - rat [R.norvegicus]
18107 I		1717	NM_022949			R.norvegicus mRNA for ribosomal protein L14

TABLE 1				Document Number: 1650775		
GLCC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
18109_A		1577	NM_012823		Annexin III (Lipocortin III)	ESTs, Weakly similar to LURT3 annexin III - rat [R.norvegicus]
18115_A		31	AA800339			ESTs
18125_S		515	AJ008787			ESTs
18136_H		737	AI102820			ESTs
18141_O		1014	AI177413		ATP synthase subunit d	ATP synthase subunit d ESTs, Weakly similar to myo-inositol-1-phosphate synthase [D.melanogaster]
						ESTs, Highly similar to ACDV_RAT ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC, MITOCHONDRIAL PRECURSOR [R.norvegicus]
18203_P		1584	NM_012891			ESTs
18235_L		758	AI104523			ESTs, Highly similar to CDC45L [M.musculus]
18237_Q		1065	AI179539			ESTs
18259_J		1280	AI236601			ESTs
18272_B		6	AA799294			ESTs, Moderately similar to KIAA0740 protein [H.sapiens]
18280_L		384	AA946361			ESTs, Highly similar to Ring3 [M.musculus]
18285_R		341	AA943791			ESTs
18316_K		499	AF072411			Rattus norvegicus FAT mRNA, complete cds
18318_S		385	AA946368			Rattus norvegicus FAT mRNA, complete cds
18323_E		556	AI012498			ESTs
18349_J		22	AA799744			ESTs

TABLE 1				Document Number 1650775		
GLQC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
18369	G	19	AA799645			Rattus norvegicus phospholemmann chloride channel mRNA, complete cds
18389	A,B,Q	9	AA799498			Rattus norvegicus brain natriuretic
18390	A,E	128	AA850038		Brain natriuretic factor	peptide (BNP) mRNA, complete cds
18418	C	969	A1176483			ESTs
						ESTs
18452	A	1630	NM_017074	Cysteine metabolism, Methionine metabolism, Nitrogen metabolism, Selenoamino acid metabolism	CTL target antigen	CTL target antigen
18453	A	1630	NM_017074	Cysteine metabolism, Methionine metabolism, Nitrogen metabolism, Selenoamino acid metabolism	CTL target antigen	CTL target antigen
18465	B,Q	1077	A180187			ESTs
18473	K	838	A1168975			ESTs
18482	H	1311	A1639151			ESTs, Highly similar to pinin [H.sapiens]
18484	L	1249	A1235349			ESTs, Highly similar to KIAA0184 [H.sapiens]
18495	B	1307	A1639042			ESTs
18501	J	1414	M31178			Rat calbindin D28 mRNA, complete cds
18522	A,E	830	A1145870			ESTs
18529	B,Q	1136	A1230716			ESTs
18580	M,P	142	AA851963			ESTs
18584	H	216	AA891694			ESTs

TABLE 1				Document Number 1650775		
GLCC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
18588 E		276	AA899635			ESTs, Moderately similar to 2020285A BRG1 protein [M.musculus]
18597 A		481	AB013732	Nucleotide sugars metabolism, Pentose and glucuronate interconversions, Starch and sucrose metabolism	HMm:UDP-glucose dehydrogenase	Rattus norvegicus mRNA for UDP-glucose dehydrogenase, complete cds
18604 N		1292	A1237124			ESTs
18606 A		1497	X53504			ESTs, Highly similar to RL12_RAT 60S RIBOSOMAL PROTEIN L12 [R.norvegicus]
18612 E.O		1092	A1228624			ESTs, Highly similar to RL23_HUMAN 60S RIBOSOMAL PROTEIN L23 [R.norvegicus]
18647 E		1435	S69316			ESTs, Weakly similar to HS9B_RAT HEAT SHOCK PROTEIN HSP 90-BETA [R.norvegicus]
18660 A		894	A1171262		cyclin G2	ESTs
18661 A		376	AA945751			ESTs
18685 L		453	AA997746	Fatty acid metabolism	dodecanoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)	dodecanoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)
18705 I		1732	NM_020103		Ly6-C antigen gene	Ly6-C antigen gene
18727 S		1685	NM_021577	Alanine and aspartate metabolism, Arginine and proline metabolism, Urea cycle and metabolism of amino groups	HHs:argininosuccinate lyase	Rat mRNA for argininosuccinate lyase, complete cds

TABLE 1				Document Number: 1650775	
GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
18742 O,S	769	A105131			ESTs, Highly similar to AF189764_1 alpha/beta hydrolase-1 [M.musculus]
18746 S	900	A1171506	Pyruvate metabolism	Malic enzyme 1, soluble	Malic enzyme 1, soluble
18747 S	1550	NM_012600	Pyruvate metabolism	Malic enzyme 1, soluble	Malic enzyme 1, soluble
18749 S	1550	NM_012600	Pyruvate metabolism	Malic enzyme 1, soluble	Malic enzyme 1, soluble
18755 C,D	1279	A1236599			ESTs
18783 N	1282	A1236746			ESTs
18792 A	662	A071177			ESTs
18795 N	1483	U95001			ESTs
18796 A	45	AA817761			ESTs
18829 H	84	AA818796			ESTs
					ESTs, Moderately similar to PLTP_MOUSE PHOSPHOLIPID TRANSFER PROTEIN PRECURSOR [M.musculus]
18837 G	901	A1171583			ESTs, Weakly similar to N-copine [M.musculus]
18854 A	1300	A1237636			Rattus norvegicus sulfotransferase subunit, complete cds
18860 A,K	861	A1169695			Rattus norvegicus mRNA for hydroxysteroid sulfotransferase subunit, complete cds
18861 A	1329	D14989	Androgen and estrogen metabolism, Sulfur	Hsp-ALCOHOL SULFOTRANSFERASE	Rattus norvegicus mRNA for hydroxysteroid sulfotransferase subunit, complete cds
18867 A	1348	D88250			Rattus norvegicus mRNA for serine protease, complete cds
18877 O	686	A072393			ESTs
18885 R	583	A1029827			ESTs, Highly similar to AF157028_1 protein phosphatase methyltransferase-1 [H.sapiens]

TABLE 1					Document Number 1650775	
GLGC Comparison ID	Core	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
18886	R	340	AA943785			ESTs, ESTs, Highly similar to AF157028.1 protein phosphatase methyltransferase-1 [H.sapiens]
18890	B,P,S	280	AA899964			ESTs
18891	B,Q,S	303	AA924598			ESTs
18900	F	1214	AI233570			ESTs, Highly similar to PSD8 HUMAN 26S PROTEASOME REGULATORY SUBUNIT S14 [H.sapiens]
18905	E	883	AI170770	Oxidative phosphorylation, Ubiquinone biosynthesis	HHs:NADH dehydrogenase (ubiquinone) Fe-S protein 2 (49KD) (NADH-coenzyme Q reductase)	ESTs, Highly similar to NADH-ubiquinone oxidoreductase NDUF-S2 subunit [H.sapiens]
18906	A,K	243	AA892561			ESTs, Moderately similar to PTD012 [H.sapiens]
18908	A	122	AA849426			ESTs
18909	A	122	AA849426			ESTs
18910	A	1182	AI232419			ESTs
18956	S	1631	NM_017075	Bile acid biosynthesis, Butanoate metabolism, Fatty acid biosynthesis (path 2), Fatty acid metabolism, Lysine degradation, Propanoate metabolism, Pyruvate metabolism, Synthesis and degradation of ketone bodies,	Acetyl-Co A acetyltransferase 1, mitochondrial	Acetyl-Co A acetyltransferase 1, mitochondrial
18960	A	1004	AI177103	Tryptophan metabolism		ESTs

TABLE 1				Document Number 1650775		
GLQC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc.ID	Pathways	Known Gene Name	UniGene Cluster Title
18962 R		574	A1013918			Rattus norvegicus TM6P1 (TM6P1) mRNA, complete cds
18974 M		319	AA925384			EST
18981 H		11	AA799523			ESTs, Moderately similar to hnRNP protein [R.norvegicus]
18990 G		1438	S72506	Glutathione metabolism	Glutathione-S-transferase, alpha type (Yc?)	Glutathione-S-transferase, alpha type (Yc?)
18996 N		1027	A1178326			ESTs
19012 J.K		918	A1172056			ESTs
19040 I		1374	J03627			ESTs
19043 F		130	AA850378			Rat S-100 related protein mRNA, complete cds, clone 42C
19044 S		386	AA946379			ESTs, Highly similar to methyl-CpG binding protein MBD2 [M.musculus]
19052 E.R		1253	A1235675			ESTs, Highly similar to methyl-CpG binding protein MBD2 [M.musculus]
19053 K		1327	D12770			ESTs
19069 A.L		339	AA943737			Rattus norvegicus mRNA for mitochondrial adenine nucleotide translocator
19073 F		34	AA800576			ESTs
19075 B.J		1275	A1236473			ESTs
19085 A.J		244	AA892598			ESTs, Moderately similar to cysteine-rich hydrophobic 1 [M.musculus]
19086 A.J		244	AA892598			ESTs
19103 A		36	AA800797			ESTs
19105 E		162	AA859230			ESTs, Highly similar to HG14 MOUSE NONHISTONE CHROMOSOMAL PROTEIN HMG-14 [M.musculus]

TABLE 1					Document Number 1650775	
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
19121 P		608	AI044101			ESTs
19150 C		8	AA739461			ESTs
19158 B		140	AA851953			ESTs, Moderately similar to hypothetical protein [H.sapiens]
19184 J		1022	AI178025			ESTs, Highly similar to TGIF_MOUSE 5'-TG-3' INTERACTING FACTOR [M.musculus]
19211 N		136	AA851329			ESTs
19230 R		646	AI059604		Serine/threonine kinase 10	ESTs
19241 I		1666	NM_019206		anti-oxidant protein 2	Serine/threonine kinase 10
19252 N			NM_019382			anti-oxidant protein 2
19255 K		1406	M15562			Rat (diabetic BB) MHC class II alpha chain RT1.D alpha (u)
19256 K		1406	M15562			Rat (diabetic BB) MHC class II alpha chain RT1.D alpha (u)
19258 O		287	AA900613			ESTs
19261 O		741	AI102943			ESTs
19264 C.D.R		743	AI103078			ESTs
19292 K		445	AA997323			EST
19298 A.D.I		1272	AI236338			ESTs, Weakly similar to NHPX_RAT NHP2/RS6 FAMILY PROTEIN
19315 E		1144	AI231010			YEL026W HOMOLOG [R.norvegicus]
19363 A.F		954	AI176247			EST
19373 N		1684	NM_021266		Hyaluronan mediated motility receptor (RHAMM)	ESTs, Moderately similar to unnamed protein product [H.sapiens]

TABLE 1					Document Number 1650775	
GLCC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
19377 I		180	AA858971			ESTs, Moderately similar to RL3_RAT
19388 F		206	AA891032			60S RIBOSOMAL PROTEIN L3 [R.norvegicus]
				Arginine and proline metabolism,Biosynthesis and degradation of glycoprotein		EST
19392 M		1592	NM_012998		Protein disulfide isomerase (Prolyl 4-hydroxylase, beta polypeptide)	Protein disulfide isomerase (Prolyl 4-hydroxylase, beta polypeptide)
19410 B,Q		268	AA893667			ESTs, Moderately similar to AC006978_1 supported by human and rodent ESTs [H.sapiens]
19411 M,P		268	AA893667			ESTs, Moderately similar to AC006978_1 supported by human and rodent ESTs [H.sapiens]
19412 B,Q		120	AA849222			ESTs, Moderately similar to AC006978_1 supported by human and rodent ESTs [H.sapiens]
19444 P		309	AA924993			ESTs
19458 E		462	AA996345			EST
19465 K		630	A045881			EST
19469 A,P		231	AA892112			ESTs, Weakly similar to proline dehydrogenase [M.musculus]
19470 A		1203	A1233266			ESTs, Weakly similar to proline dehydrogenase [M.musculus]
19476 O		1188	A1232612			ESTs
19503 P		116	AA848639			ESTs, Moderately similar to vascular endothelial growth factor D [M.musculus]
19508 A		1114	A1229698			EST

TABLE 1					Document Number: 1650775	
GLCC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
19512 M		855	A1169612			Rattus norvegicus adipocyte lipid-binding protein (ALBP) mRNA, complete cds
19513 R		1100	A1229035			ESTs
19566 E		112	AA819879			ESTs, Highly similar to ATP binding protein [H.sapiens]
19591 S		559	A012747			ESTs
19605 E.L		97	AA819172			EST
19641 J		663	A1071181			EST
19650 H		486	AF016387			ESTs, Rattus norvegicus retinoid X receptor gamma (RXRgamma) mRNA, partial cds
19669 R		1740	NM_022944			Rattus norvegicus mRNA for SH2-containing inositol phosphatase 2 (SHIP2), complete cds
19671 B.Q		1656	NM_017309		protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I)	protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I)
19678 A		1733	NM_021653		Thyroxine deiodinase, type I	Rat mRNA for type I thyroxine deiodinase
19679 A		1733	NM_021653		Thyroxine deiodinase, type I	Rat mRNA for type I thyroxine deiodinase
19715 M		1662	NM_019190		membrane cofactor protein	membrane cofactor protein
19728 O		872	A1170394			ESTs
19729 A		87	AA818910			ESTs
19732 A.G		1262	A1236066			ESTs
19762 R		272	AA899113			EST
19768 I		237	AA892373			ESTs
19787 H		1304	A1638994			ESTs

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GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name
19824 O	1688	NM_021750	Taurine and hypotaurine metabolism	HHs:cysteine sulfinic acid decarboxylase-related protein 2
19825 O	1688	NM_021750	Taurine and hypotaurine metabolism	HHs:cysteine sulfinic acid decarboxylase-related protein 2
19830 A	853	AI169529		
19843 A	1308	AI639055		
19909 A	1315	AI639310		
19940 C	1254	AI235689		
19952 A	1310	AI639108		
20016 B	1312	AI639158		
20035 A	1689	NM_021754		
20038 S	278	AA899797		
20041 K	787	AI112161		
20063 E.L	313	AA925063		
20062 C	1316	AI639488		
20088 A	246	AA892666		
20090 R	1690	NM_021757		
20119 P	1033	AI178533		

TABLE 1				Document Number: 1650775		
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
20134	P		1692 NM_021852			Rattus norvegicus EH domain binding protein epsin 2 mRNA, complete cds
20161	A,B		1691 NM_021836			R.norvegicus pJunB gene
20200	M		1693 NM_022194			Rat interleukin 1 receptor antagonist gene, complete cds
20282	H		1648 NM_017274	Glycerolipid metabolism	glycerol-3-phosphate acyltransferase, mitochondrial	glycerol-3-phosphate acyltransferase, mitochondrial
20299	A,D		1694 NM_022220			Rattus norvegicus gene for L-gulonogamma-lactone oxidase
20350	L,Q		1186 AI232552			EST
20354	B,N,Q		1404 M14369		K-kininogen, differential splicing leads to HMW Kngk	K-kininogen, differential splicing leads to HMW Kngk
20380	E,G		1330 D16102	Glycerolipid metabolism	glycerol kinase	Rattus norvegicus mRNA for ATP-stimulated glucocorticoid-receptor translocaton promoter, complete cds
						ESTs, Moderately similar to SYM_HUMAN METHIONYL-TRNA SYNTHETASE [H.sapiens]
20397	A,E		1151 AI231226			Rattus norvegicus JE/MCP-1 mRNA, complete cds
20449	A,C,I		1494 X17053		Small inducible gene JE	ESTs
20456	A,C		1355 H31144			Rattus norvegicus mRNA for organic anion transporting polypeptide 4 (slc21a10 gene)
20502	A,F		370 AA945533			Rattus norvegicus mRNA for organic anion transporting polypeptide 4 (slc21a10 gene)
20503	A,C,E		864 AI169779			Rattus norvegicus mRNA for organic anion transporting polypeptide 4 (slc21a10 gene)

TABLE 1					Document Number: 1650775	
GLCC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
				Glycolysis/ Gluconeogenesis, Purine metabolism, Pyruvate metabolism		
20513 A		1554	NM_012624		Pyruvate kinase, liver and RBC	Pyruvate kinase, liver and RBC
20522 P		224	AA891842			ESTs, Moderately similar to podocalyxin [R.norvegicus]
20523 C,P		224	AA891842			ESTs, Moderately similar to podocalyxin [R.norvegicus]
20529 F,M,P		1644	NM_017208		lipopolysaccharide binding protein	lipopolysaccharide binding protein
						Rattus norvegicus carnitine octanoyltransferase mRNA, complete cds
20555 G		1458	U26033			
					sodium channel, voltage-gated, type I, beta polypeptide	sodium channel, voltage-gated, type I, beta polypeptide
20579 O		1654	NM_017288		Protein 9 Ka homologous to calcium-binding protein	Protein 9 Ka homologous to calcium-binding protein
20589 I		1553	NM_012618	Alanine and aspartate metabolism; Arginine and proline metabolism; Urea cycle and metabolism of amino groups		
20597 S		1489	X12459		Arginosuccinate synthetase 1	Arginosuccinate synthetase 1
						ESTs, Highly similar to SRPR_HUMAN SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT [H.sapiens]
20644 I		996	AI176990			Cytochrom P450
20651 P		1460	U36992		Cytochrom P450	ESTs
20684 C		1361	H32977			ESTs
20694 A		442	AA997048			ESTs

TABLE 1					Document Number: 1650775	
GLC/ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
20698 N		1519	X86561			
20701 A,B,F,Q		197	AA875097			Rat alpha-fibrinogen mRNA, 3' end
20705 A,D		1541	NM_012541	Fatty acid metabolism, Tryptophan metabolism	Cytochrome P450, subfamily I (aromatic compound-inducible), member A2 (Q42, form d)	Cytochrome P450, subfamily I (aromatic compound-inducible), member A2 (Q42, form d)
20707 A,D,K		1481	U88036			Rattus norvegicus brain digoxin carrier protein mRNA, complete cds
20708 C,F		476	AB006461			Rattus norvegicus mRNA for NORBIN, complete cds
20711 E,K		1622	NM_016999	Fatty acid metabolism, Tryptophan metabolism	Cytochrome P450, subfamily IVB, polypeptide 1	Cytochrome P450, subfamily IVB, polypeptide 1
20713 K		1622	NM_016999	Fatty acid metabolism, Tryptophan metabolism	Cytochrome P450, subfamily IVB, polypeptide 1	Cytochrome P450, subfamily IVB, polypeptide 1
20714 K		1622	NM_016999	Fatty acid metabolism, Tryptophan metabolism	Cytochrome P450, subfamily IVB, polypeptide 1	Cytochrome P450, subfamily IVB, polypeptide 1
20715 E,N		1622	NM_016999	Fatty acid metabolism, Tryptophan metabolism	Cytochrome P450, subfamily IVB, polypeptide 1	Cytochrome P450, subfamily IVB, polypeptide 1
20734 A		1672	NM_019283		antigen identified by monoclonal antibodies 4F2	antigen identified by monoclonal antibodies 4F2
20735 A,C,D		1672	NM_019283		antigen identified by monoclonal antibodies 4F2	antigen identified by monoclonal antibodies 4F2
20741 F		502	AF084186			R norvegicus mRNA for alpha II spectrin

TABLE 1				Document Number 1650775		
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
				Alanine and aspartate metabolism, Arginine and proline metabolism, Cysteine metabolism, Glutamate metabolism, Phenylalanine metabolism, Phenylalanine, tyrosine and tryptophan biosynthesis, Tyrosine metabolism	Glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase, cytosolic) see also D1Mgh12	Glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase, cytosolic) see also D1Mgh12
20744 K		1545	NM_012571		Cyclin G1	Cyclin G1
20755 I		1587	NM_012923		Cyclin G1	Cyclin G1
20757 A		1587	NM_012923		Cyclin G1	Rattus norvegicus protein arginine N-methyltransferase (PRMT1) mRNA, complete cds
20772 A,F		1468	U60882			ESTs, Moderately similar to HS9B RAT HEAT SHOCK PROTEIN HSP 90-BETA [R.norvegicus]
20795 J		355	AA944397	egf, epo, il2, il3, il6, insulin, inter	Murine leukemia viral (v-rat-1) oncogene homolog 1 (3611-MSV)	Murine leukemia viral (v-rat-1) oncogene homolog 1 (3611-MSV)
20799 H		1405	M15428	act6-1, ngf, pdgf, tpo		Rattus norvegicus mRNA for APEX nuclease, complete cds
20801 A,I		1723	NM_024148		Apurinic/apyrimidinic endonuclease 1	Rattus norvegicus Sprague-Dawley transketolase mRNA, complete cds
20803 K		1707	NM_022592	Pentose phosphate cycle	HMm:transketolase	Rattus norvegicus Sprague-Dawley transketolase mRNA, complete cds
20804 K		1707	NM_022592	Pentose phosphate cycle	HMm:transketolase	ESTs, Highly similar to RL1X RAT 60S RIBOSOMAL PROTEIN L18A [R.norvegicus]
20810 A		1493	X14181			

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GLQC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc. ID	Pathways	Known Gene Name	Unigene Cluster Title
20817	G		558 A012589	Glutathione metabolism	glutathione S-transferase, pl 2	glutathione S-transferase, pl 2
20818	G		1485 X02904	Glutathione metabolism	glutathione S-transferase, pl 2	glutathione S-transferase, pl 2
20843	C,D		13 AA799545			EST's, Weakly similar to TCPA, RAT T-COMPLEX PROTEIN 1, ALPHA SUBUNIT [R.norvegicus]
						EST's, Highly similar to RL2B, HUMAN 60S RIBOSOMAL PROTEIN L23A [R.norvegicus]
20846	E,N		1147 A1231140			Rat mRNA for myosin regulatory light chain (RLC)
20849	F,I		1487 X05566		acyl-CoA hydrolase	acyl-CoA hydrolase
20851	E		1614 NM_013214		Carnitine palmitoyltransferase 1 beta, muscle isoform	Carnitine palmitoyltransferase 1 beta, muscle isoform
20855	S		1613 NM_013200	Fatty acid metabolism, Glycerolipid metabolism	Carnitine palmitoyltransferase 1 beta, muscle isoform	Carnitine palmitoyltransferase 1 beta, muscle isoform
20856	S		1613 NM_013200	Fatty acid metabolism, Glycerolipid metabolism	Carnitine palmitoyltransferase 1 beta, muscle isoform	Carnitine palmitoyltransferase 1 beta, muscle isoform
20864	G,K,P		1615 NM_013215		afatoxin B1 aldehyde reductase	afatoxin B1 aldehyde reductase
						EST's, Highly similar to RS19, RAT 40S RIBOSOMAL PROTEIN S19 [R.norvegicus]
20873	G		1000 A1177042			EST's, Moderately similar to KIAA0952 protein [H.sapiens]
20874	A		1116 A1229789			R.norvegicus mRNA for pl 6.1 esterase (ES-10)
20879	I		1511 X65296			Solute carrier 16 (monocarboxylic acid transporter), member 1
20889	A		1563 NM_012716			EST's, Highly similar to CGI-117 protein [H.sapiens]
20891	A,C,I		852 A1169337			EST's, Highly similar to Copa protein [M.musculus]
20897	I		945 A1175812			

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GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
20914 B	1412	M23995		Aldehyde dehydrogenase 1 (phenobarbital inducible)	Aldehyde dehydrogenase 1 (phenobarbital inducible)
20915 K,Q	1730	NM_0117272		Aldehyde dehydrogenase 1 (phenobarbital inducible)	Aldehyde dehydrogenase 1 (phenobarbital inducible)
20930 E	473	AB004096	Fatty acid metabolism, Tryptophan metabolism	Cytochrom P450 Lanosterol 14 alpha-demethylase	Cytochrom P450 Lanosterol 14 alpha-demethylase
20950 I	7	AA799323			ESTs, Moderately similar to PLEK_HUMAN PLECKSTRIN [H.sapiens]
20971 H	15	AA799576			ESTs, Weakly similar to nucleolar RNA helicase II/Gu [M.musculus]
20975 H	16	AA799599			ESTs
20980 E	18	AA799633			ESTs
20983 F	619	A0044900		Acyl CoA synthetase, long chain	Acyl CoA synthetase, long chain
20986 G	260	AA893242		Acyl CoA synthetase, long chain	Acyl CoA synthetase, long chain
20993 R	1041	A1178741			ESTs
					ESTs, Weakly similar to serine protease [R.norvegicus]
20998 S	24	AA799803			
21010 S	318	AA925306	Alanine and aspartate metabolism	HMm: carnitine acetyltransferase	ESTs
21014 P	1376	J03914	Glutathione metabolism	Glutathione-S-transferase, mu type 2 (Yb2)	Glutathione-S-transferase, mu type 2 (Yb2)
21025 A	163	AA859241		synaptotagmin 2 binding protein	Rattus norvegicus NPW16 mRNA, complete cds
21039 B	1373	J03190	Glycine, serine and threonine metabolism	HHs: aminolevulinic, delta-, synthase 1	Rat 5-aminolevulinic synthase mRNA, complete cds
21040 E	546	A011734	Glycine, serine and threonine metabolism	HHs: aminolevulinic, delta-, synthase 1	Rat 5-aminolevulinic synthase mRNA, complete cds

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GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
21060 I		547	A011746			ESTs, Weakly similar to BACR7C10.a [D.melanogaster]
21068 E		943	A1175675			ESTs, Highly similar to RB24 MOUSE RAS-RELATED PROTEIN RAB-24 [M.musculus]
21075 P		1706	NM_022584	Fatty acid metabolism, Propanoate metabolism, Valine, leucine and isoleucine degradation, beta-Alanine metabolism	thioredoxin reductase 2	Rattus norvegicus thioredoxin reductase (TrxR2) mRNA, nuclear gene encoding mitochondrial protein, complete cds
21078 K		1617	NM_016986		Acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight-chain	Acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight-chain
21088 A,F		966	A1176472			ESTs
21091 E		1289	A236972			ESTs, Weakly similar to predicted using Genefinder [C.elegans]
21097 A,H,N		1400	M12112		Angiotensinogen	Rat angiotensinogen (PAT) gene
21098 N		344	AA943892		Angiotensinogen	Rat angiotensinogen (PAT) gene
21125 A		114	AA848437			ESTs
21130 J		959	A1176298			ESTs
21150 A		119	AA848826			ESTs
21157 A		383	AA946189			ESTs
21164 O,S		810	A1137488			ESTs
21175 H		768	A105113			ESTs
21184 K		709	A101205			ESTs
21209 A,E		913	A117172			ESTs
21228 K,M		615	A044404			ESTs

TABLE 1					Document Number: 1650775	
GLCC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
21238 K		1719	NM_024125	il6.interact6-1	Liver activating protein (LAP, also NF-IL6, nuclear factor-IL6, previously designated TCF5)	Rat sfb mRNA for silencer factor B
21256 Q		1029	AI178491			ESTs
21275 L		125	AA849796			ESTs
21281 B,E,M		1231	AI234090	Arginine and proline metabolism, Glycine, serine and threonine metabolism, Histidine metabolism, Phenylalanine metabolism, Tryptophan metabolism, Tyrosine metabolism		ESTs, Moderately similar to hypothetical protein [H.sapiens]
21285 P		126	AA849898			EST
21305 G		258	AA893082			ESTs
21321 H		1227	AI233902			ESTs
21341 A,S		129	AA850195			ESTs
21354 S		277	AA899721			ESTs
21380 J		35	AA800739			ESTs, Weakly similar to /prediction
21382 N		375	AA945708			ESTs
				Arginine and proline metabolism, Glycine, serine and threonine metabolism, Histidine metabolism, Phenylalanine metabolism, Tryptophan metabolism, Tyrosine metabolism		
21396 A		1612	NM_013198	Monoamine oxidase B	Monoamine oxidase B	Monoamine oxidase B
21414 P		1255	AI235842			ESTs
21416 I		37	AA800962			ESTs, Highly similar to TAL1_MOUSE
21421 N		1664	NM_019196		multiple PDZ domain protein	TALIN [M.musculus]
21443 P,Q		1671	NM_019262		complement component 1, q subcomponent, beta polypeptide	complement component 1, q subcomponent, beta polypeptide

TABLE 1				Document Number 1650775		
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
21444 Q		1671	NM_019262		complement component 1, q subcomponent, beta polypeptide	complement component 1, q subcomponent, beta polypeptide
21445 M,P		1388	L18948			Rattus norvegicus intracellular calcium-binding protein (MRP14) mRNA, complete cds
21458 C		311	AA925049			ESTs
21467 N		951	AI176061			ESTs, Weakly similar to tazarotene-induced gene 2 [H.sapiens]
21471 A		137	AA851343			ESTs
21535 R		1097	A228729			ESTs
21567 R		707	AI101159			ESTs
21570 B		762	AI104683			ESTs
21574 N		146	AA852038	Biosynthesis and degradation of glycoprotein		ESTs
21575 E		1499	X55298		HHs:ribophorin II	Rat ribophorin II mRNA
21586 G,I		1521	X97772			R.norvegicus mRNA for D-3-phosphoglycerate dehydrogenase
21657 B		1507	X61381			Rattus norvegicus interferon-inducible protein variant 10 mRNA, complete cds
21660 M		863	AI169751			Rattus norvegicus interferon-inducible protein variant 10 mRNA, complete cds
21661 M		968	AI176479			Rattus norvegicus interferon-inducible protein variant 10 mRNA, complete cds
21663 B		1635	NM_017126			Rattus norvegicus interferon-inducible protein variant 10 mRNA, complete cds
21672 C		222	AA891789		ferredoxin 1	ferredoxin 1
21682 P,Q		1609	NM_013154		CCAAT/enhancerbinding, protein (C/EBP) delta	CCAAT/enhancerbinding, protein (C/EBP) delta
21683 P		1609	NM_013154		CCAAT/enhancerbinding, protein (C/EBP) delta	CCAAT/enhancerbinding, protein (C/EBP) delta

TABLE 1					Document Number: 1650775	
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
21695	A,I	240	AA892506			ESTs, Weakly similar to coronin-like protein [R.norvegicus]
21696	C	1724	NM_024152			Rattus norvegicus ADP-ribosylation factor 6 mRNA, complete cds
21707	A,C,E,N	176	AA859722			ESTs
21709	Q	1334	D29683		Hsp-ENDORHELIN-CONVERTING ENZYME 1	Rat mRNA for endothelin-converting enzyme, complete cds
21717	E	131	AA850480			ESTs
21740	B,M,Q	986	A1176810			ESTs
21798	K	329	AA926365			ESTs, Moderately similar to AF151827_1 CGI-69 protein [H.sapiens]
21799	E	730	A102576			ESTs
21818	I	491	AF036537			Rattus norvegicus homocysteine respondent protein HCYP2 mRNA, complete cds
21823	E	1119	A1229906			ESTs
21893	E	1302	A1237713			ESTs, Moderately similar to Y101_HUMAN HYPOTHETICAL PROTEIN KIAA0101 [H.sapiens]
21909	H	210	AA891161			ESTs
21950	G	570	A1013861			Rattus norvegicus 3-hydroxyisobutyrate mRNA, 3' end
21976	R	379	AA946011			ESTs
21977	A,G	1432	S46785			Rattus norvegicus insulin-like growth factor binding protein complex acid-labile subunit gene, complete cds

TABLE 1				Document Number: 1650775	
GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
21978 A.M	298	AA924289			Rattus norvegicus insulin-like growth factor binding protein complex acid-labile subunit gene, complete cds
21980 H	264	AA893454			ESTs
22038 A.C.D	1297	A1237609			ESTs
22042 P	390	AA946476			ESTs
22046 S	331	AA942726			ESTs
22051 E	275	AA899498			ESTs, Weakly similar to predicted using Genfinder [C.elegans]
22077 A	1003	A1177099			ESTs, Highly similar to serine protease [H.sapiens]
22099 A	727	A102258			ESTs, Moderately similar to B164_MOUSE BRAIN PROTEIN I54 [M.musculus]
22124 J	223	AA891790			ESTs
22135 R	887	A1170821			ESTs, Weakly similar to predicted using Genfinder [C.elegans]
22151 B.E.Q	521	A1009115			ESTs
22177 J	753	A103730			ESTs
22197 A.C	1031	A1178527			ESTs
22204 K	886	A1170820			ESTs
22212 A	1268	A1236294			ESTs, Highly similar to translation initiation factor eIF6 [M.musculus]
22224 S	323	AA925869			ESTs
22235 L	294	AA924152			ESTs, Moderately similar to AF135422_1 GDP-mannose pyrophosphorylase A [H.sapiens]
22266 E.K	373	AA945601			ESTs

TABLE 1					Document Number: 1650775	
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
22321	B,I,M,Q	1372	J02962			Rat IgE binding protein mRNA, complete cds
22338	A	345	AA943896			ESTs
22368	A,Q	348	AA944157			ESTs
22370	S	349	AA944158			ESTs
22375	R	1121	AI230046			ESTs
22379	L	1156	AI231448	Glycolysis / Gluconeogenesis, Pentose phosphate cycle, Starch and sucrose metabolism	Glucose phosphate isomerase	ESTs, Highly similar to GPI_MOUSE GLUCOSE-6-PHOSPHATE ISOMERASE [M.musculus]
22392	S	351	AA944269			ESTs, Weakly similar to es 64 [M.musculus]
22395	A	352	AA944289			ESTs
22397	F	353	AA944304			ESTs
22412	E	1702	NM_022392			Rattus norvegicus growth response protein (CL-6) mRNA, complete cds
22416	S	354	AA944380			ESTs
22432	A,C	895	AI171263			ESTs, Highly similar to FBRL_MOUSE FIBRILLARIN [M.musculus]
22443	J	1284	AI236761			ESTs
22457	A	358	AA944572			ESTs, Weakly similar to T2D7_RAT TRANSCRIPTION INITIATION FACTOR TFIIID 31 KD SUBUNIT [R.norvegicus]
22487	A,F,H	731	AI102578			ESTs, Highly similar to I49523 Mouse primary response gene B94 mRNA, 3'end - mouse [M.musculus]
22503	L	359	AA944823			ESTs
22512	M,P	1531	NM_012488		Alpha-2-macroglobulin	Alpha-2-macroglobulin
22513	F,M	1531	NM_012488		Alpha-2-macroglobulin	Alpha-2-macroglobulin

TABLE 1				Document Number 1650775		
GLCC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
22514	M,P	1531	NM_012488		Alpha-2-macroglobulin	Alpha-2-macroglobulin
22515	M	1531	NM_012488		Alpha-2-macroglobulin	Alpha-2-macroglobulin
22516	M,P	796	AI113046		Alpha-2-macroglobulin	Alpha-2-macroglobulin
22531	E	361	AA944943			ESTs
22534	E	310	AA925045			ESTs
				Glyoxylate and dicarboxylate metabolism,Pyruvate metabolism		
22540	R	304	AA924630		HHs:glyoxylate reductase/hydroxypyruvate reductase	ESTs, Weakly similar to SERA_RAT D-3 PHOSPHOGLYCERATE DEHYDROGENASE [R.norvegicus]
22548	L	364	AA945031			ESTs
22554	A,E,G,O	366	AA945076		Hydroxyacid oxidase 1 (glycolate oxidase)	ESTs
22558	A,E	368	AA945123			EST
22559	A,D	839	AI169007			ESTs
22566	E	1007	AI177122			ESTs
22569	A	1073	AI179979			ESTs
22570	R	369	AA945238			ESTs
22582	A,G	1605	NM_013120		Glucokinase regulatory protein	Glucokinase regulatory protein
22598	M	811	AI137506			ESTs, Weakly similar to SPI-2 serine protease inhibitor [R.norvegicus]
						Rattus norvegicus putative peroxisomal 2,4-dienoyl-CoA reductase (DCR-AKL) mRNA, complete cds
22603	E	494	AF044574			ESTs
22619	B,E,Q	531	AI009825			ESTs
22620	S	316	AA925258			ESTs
22625	J	374	AA945704			ESTs
22679	A	332	AA942731			ESTs
22681	J	357	AA944413			ESTs
22683	A	970	AI176484			ESTs

TABLE 1				Document Number: 1650775		
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
22695	H	1032	AI178531			ESTs
22713	K	378	AA945904			ESTs
22717	L	1257	AI235948			ESTs, Highly similar to entactin [R.norvegicus]
22722	O	804	AI137211			ESTs
22725	Q	283	AA900506			ESTs, Highly similar to TS24_MOUSE PROTEIN TSG24 [M.musculus]
22737	S	465	AA998660			ESTs
22770	A	387	AA946428			ESTs
22806	E,Q	551	AI012174			ESTs, Moderately similar to hypothetical protein [H.sapiens]
22835	L	1079	AI180367			Rattus norvegicus small zinc finger-like protein (TIM10) mRNA, complete cds
22840	N	528	AI009676			ESTs
22862	H	227	AA891944			ESTs
22876	C	917	AI172041			ESTs, Moderately similar to CGH-137 protein [H.sapiens]
22877	A,C,D	1045	AI178819			ESTs, Moderately similar to CGH-137 protein [H.sapiens]
22897	P	290	AA901107			ESTs
22898	L,P	290	AA901107			ESTs
22906	L,N	944	AI175790			ESTs
22918	B,Q	29	AA800243			ESTs, Moderately similar to cell death activator CIDE-A [M.musculus]
22928	A,F	328	AA926262			ESTs
22929	A,L	670	AI071578			ESTs
22930	A	670	AI071578			ESTs
22931	A	777	AI105417			ESTs

TABLE 1					Document Number 1650775	
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
22957	R	764	A1104897		HMM-mitogen activated protein kinase kinase 3	ESTs, Moderately similar to meningioma expressed antigen 11 [H.sapiens]
22961	E	1064	A1179519			ESTs
22966	B	1128	A1230320			ESTs
23000	H	178	AA859933			ESTs
23005	F,P	334	AA942770			ESTs
23013	I	1137	A1230743			ESTs, Weakly similar to ACTC_HUMAN ACTIN, ALPHA CARDIAC
23030	L	305	AA924763			[R.norvegicus]
23032	K	976	A1176596			ESTs
23033	G	179	AA859938			ESTs
23043	N	1051	A1178968			ESTs, Weakly similar to URB1_RAT DNA BINDING PROTEIN URE-B1 [R.norvegicus]
23044	A,H	490	AF034218			Rattus norvegicus hyaluronidase (Hyal2)
23047	H	230	AA892027			mRNA, complete cds
23075	A	844	A1169166			ESTs
23077	H	1015	A1177489			ESTs
23082	A	980	A1176648			ESTs
23089	C	789	A1112365			ESTs, Highly similar to mm-Mago [M.musculus]
23106	Q,R	825	A1145081		Mini chromosome maintenance deficient 4 homolog (S. cerevisiae)	ESTs, Highly similar to cell division control protein CDC21 [H.sapiens]
23120	C,D	1070	A1179857			ESTs, Weakly similar to UBSD_RAT UBIQUITIN-CONJUGATING ENZYME E2-17 KD 4 [R.norvegicus]

TABLE 1					Document Number 1650775	
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
23125	B,Q	1172	A032286			ESTs
23128	E	561	A013011			ESTs
23139	H	1076	A180040			ESTs
23180	C,L	960	A176319		HMM:nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, beta	Rattus norvegicus I-kappa-B-beta mRNA, complete cds
23170	E	850	A169317			ESTs, Weakly similar to C43H8.1 [C.elegans]
23173	I	312	AA925057			ESTs, Highly similar to CRIP_MOUSE CYSTEINE-RICH INTESTINAL PROTEIN [R.norvegicus]
23182	F,N	1141	A230981			ESTs
23183	O	819	A114586			Rattus norvegicus eveclin-1 (EV11) mRNA, complete cds
23184	C	974	A176554			ESTs
23220	O	1319	AJ000347	Sulfur metabolism	HMM:bisphosphate 3'-nucleotidase 1	Rattus norvegicus mRNA for 3'(2'),5'-bisphosphate nucleotidase
23229	C	1229	A234038			ESTs
23230	A,H,N	1266	A236146			ESTs
23243	E	138	AA851803			ESTs
23245	Q	1086	A1179570			ESTs
23260	C,D	856	A169617			ESTs, Highly similar to Bop1 [M.musculus]
23281	A,C,D	314	AA925145			ESTs
23299	C	989	A1176839			ESTs
23302	I,N	1516	X78949	Arginine and proline metabolism	HMM:procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide	R.norvegicus mRNA for prol 4-hydroxylase alpha subunit

TABLE 1					Document Number 1650775	
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
23304 E		1153	A1231310	Arginine and proline metabolism	HMM:procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide	R.norvegicus mRNA for prolyl 4-hydroxylase alpha subunit
23315 E,R		239	AA892425			ESTs
23321 A		247	AA892821			Rattus norvegicus air mRNA for androgen-inducible aldehyde reductase, complete cds
23322 A		247	AA892821			Rattus norvegicus air mRNA for androgen-inducible aldehyde reductase, complete cds
23324 E		181	AA859980			ESTs, Weakly similar to TCPA_RAT 1-COMPLEX PROTEIN 1, ALPHA
23325 A		928	A1172405			SUBUNIT [R.norvegicus]
23331 J		1210	A1233457			ESTs
						ESTs, Highly similar to Mlark [M.musculus]
23337 E,O		520	A1009096			Rattus norvegicus double-stranded RNA binding protein p74 mRNA, complete cds
23362 O		1616	NM_013216		Ras homolog enriched in brain	Ras homolog enriched in brain
23380 A		141	AA851961			ESTs
23390 D,G		927	A1172328			ESTs, Weakly similar to TCPA_RAT 1-COMPLEX PROTEIN 1, ALPHA
23435 C		1112	A1229502			SUBUNIT [R.norvegicus]
23437 A,O		661	A1071166			ESTs, Highly similar to KIAA0601 protein [H.sapiens]
23438 C,J		745	A1103101			ESTs
						ESTs, Highly similar to F25965 1 [H.sapiens]

TABLE 1					Document Number 1650775	
GLGC Comparison ID	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title	
23445 A,D,F	1571 NM_012792			Flavin-containing monooxygenase 1	Flavin-containing monooxygenase 1	
23448 B	315 AA925167				ESTs	
23449 B,Q	987 A1176828				ESTs	
23491 H,N,O	1681 NM_019359			acidic calponin	acidic calponin	
23494 N	888 A1170967				ESTs	
23499 A	393 AA955249				EST	
23500 A,S	183 AA860010				ESTs	
23511 A	1697 NM_022294				ESTs	
					ESTs, Highly similar to S23B_HUMAN PROTEIN TRANSPORT PROTEIN SEC23 HOMOLOG ISOFORM B [H.sapiens]	
23515 L	1063 A1179498					
23522 A,F	1552 NM_012615		Arginine and proline metabolism,Urea cycle and metabolism of amino groups	Ornithine decarboxylase	Ornithine decarboxylase	
			Arginine and proline metabolism,Urea cycle and metabolism of amino groups	Ornithine decarboxylase	Ornithine decarboxylase	
23523 A	1552 NM_012615				ESTs	
23555 M,P	394 AA955443				ESTs, Weakly similar to NDKA_RAT NUCLEOSIDE DIPHOSPHATE KINASE A [R.norvegicus]	
23558 A	400 AA956170				ESTs	
23567 J	1042 A1178746				ESTs	
23584 A,B	392 AA955071				ESTs	
23587 J	977 A1176598				ESTs	

TABLE 1					Document Number 1650775	
GLGC ID	Companion Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
23606	H,N	1714	NM_022867			Rattus norvegicus microtubule-associated proteins 1A and 1B light chain 3 subunit mRNA, complete cds
23608	E	1201	AI233190			Rattus norvegicus microtubule-associated proteins 1A and 1B light chain 3 subunit mRNA, complete cds
23612	A	880	AI170751			ESTs
23626	N	395	AA955540			ESTs
23627	S	628	AI045624			ESTs, Moderately similar to AF151890.1 CGI-132 protein [H.sapiens]
23633	A	706	AI011130			ESTs
23651	I	1582	NM_012881		Sialoprotein (osteopontin)	Sialoprotein (osteopontin)
23656	R	616	AI045533			ESTs
23678	C	1674	NM_019290		B-cell translocation gene 3	B-cell translocation gene 3
23679	A,C,D,F	1674	NM_019290		B-cell translocation gene 3	B-cell translocation gene 3
23698	E	1532	NM_012489		Acetyl-CoA acyltransferase, 3-oxo acyl-CoA thiolase A, peroxisomal	Acetyl-CoA acyltransferase, 3-oxo acyl-CoA thiolase A, peroxisomal
23709	H,K	1603	NM_013113		ATPase Na+/K+ transporting beta 1 polypeptide	ATPase Na+/K+ transporting beta 1 polypeptide
23710	H	1135	AI230614		ATPase Na+/K+ transporting beta 1 polypeptide	ATPase Na+/K+ transporting beta 1 polypeptide
23711	H	1603	NM_013113		ATPase Na+/K+ transporting beta 1 polypeptide	ATPase Na+/K+ transporting beta 1 polypeptide
23762	R	404	AA956431			ESTs, Highly similar to Lsm5 protein [H.sapiens]
23767	A	1295	AI237207			ESTs
23843	E,R	412	AA957410			ESTs
23847	B	405	AA956723			EST

TABLE 1				Document Number 1650775		
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
23854	G,I	1514	X78327			R.norvegicus (Sprague Dawley) ribosomal protein L13 mRNA
23855	B,C	1287	A1236773			ESTs
23868	F	1543	NM_012551		Early growth response 1	Early growth response 1
23869	F	1543	NM_012551		Early growth response 1	Early growth response 1
23872	F	1543	NM_012551		Early growth response 1	Early growth response 1
				Arginine and proline metabolism, Ascorbate and aldarate metabolism, Bile acid biosynthesis, Butanoate metabolism, Fatty acid metabolism, Glycerolipid metabolism, Histidine metabolism, Lysine degradation, Phenylalanine metabolism, Propanoate metabolism, Pyruvate metabolism		
23884	A	1422	M73714		aldehyde dehydrogenase 4, liver microsomal (class 3)	Rat microsomal aldehyde dehydrogenase mRNA, complete cds
23885	E	866	A1170007			ESTs
23888	I	241	AA892520			ESTs
23889	M	241	AA892520			ESTs
23890	B	406	AA956864			ESTs
23945	F	409	AA957071			ESTs, Highly similar to Bcl-2-interacting protein beclin [H.sapiens]
23955	A	1103	A1229178			ESTs
23961	A,D	1640	NM_017181	Tyrosine metabolism	fumarylacetoacetate hydrolase	fumarylacetoacetate hydrolase
23987	O	1496	X51615			ESTs
23989	B,Q	1072	A1179953			ESTs
24012	M,Q	411	AA957335			ESTs

TABLE 1				Document Number:1650775		
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
24024	Q	496	AF052695			Rattus norvegicus p55CDC mRNA, complete cds
24049	G	1010	AI177341			ESTs, Highly similar to CGI-10 protein [H.sapiens]
24051	L	414	AA957452			EST
24079	H	935	AI175423			ESTs
24112	O	514	AI008773			ESTs
24126	R	415	AA957708			ESTs
24146	E	859	AI169688			ESTs, Weakly similar to hypothetical protein [H.sapiens]
24161	E	150	AA858588			ESTs
24162	A	847	AI169279			ESTs
24200	N	555	AI012356			ESTs
24219	A	1395	L27843		protein tyrosine phosphatase 4a1	Rattus norvegicus tyrosine phosphatase (PRL-1) mRNA, complete cds
24227	L	871	AI170385			ESTs
24228	M	30	AA800318			ESTs, Weakly similar to A1AT_RAT ALPHA-1-ANTIPROTEINASE PRECURSOR [R.norvegicus]
24234	J	1469	U63923			Rattus norvegicus NADPH-dependent thioredoxin reductase (TRR1) mRNA, complete cds
24235	A,D,J	213	AA891286			Rattus norvegicus NADPH-dependent thioredoxin reductase (TRR1) mRNA, complete cds
24236	C,L	967	AI176473			ESTs
24237	F,M	44	AA817726			ESTs

TABLE 1				Document Number: 1650771		
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
24246 G		419	AA963703			ESTs, Highly similar to cell cycle protein p38-2G4 homolog [H sapiens]
24264 A		1593	NM_012999		Subtilisin - like endoprotease	Subtilisin - like endoprotease
24268 E		924	AI172281			ESTs
24284 A		1715	NM_022869			Rattus norvegicus nucleolar phosphoprotein of 140kD, Nopp140 mRNA, complete cds
24289 B,Q		399	AA955986	Galactose metabolism	Galactokinase	ESTs, Highly similar to galactokinase [M.musculus]
24296 E		1360	H32867			ESTs, Highly similar to steroidogenic acute regulatory protein [R.norvegicus]
24321 A,D,G		1178	AI232340			ESTs
24323 P		763	AI104798			ESTs, Moderately similar to GTM1_RAT GLUTATHIONE S-TRANSFERASE YB1 [R.norvegicus]
24367 R		401	AA956247			EST
24368 R		1080	AI180392			ESTs, Highly similar to AF114169_1 nucleotide-binding protein short form [M.musculus]
24369 R		346	AA944011			ESTs, Highly similar to AF114169_1 nucleotide-binding protein short form [M.musculus]
24375 A,D		766	AI104979			ESTs, Highly similar to AF114169_1 nucleotide-binding protein short form [M.musculus]
24381 S		403	AA956301			ESTs, Moderately similar to nucleolar protein p40 [H sapiens]
24388 C,D,I,R		1286	AI236772			ESTs
24434 A		1710	NM_022704			ESTs
24442 O		1708	NM_022667			Rat mannose-binding protein C (liver) mRNA, complete cds
						Rat matrin F/G mRNA, complete cds

TABLE 1				Document Number 1650775		
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
24453 F		1560	NM_012690		P-glycoprotein 3/ multidrug resistance 2, P-glycoprotein/multidrug resistance 1	P-glycoprotein 3/ multidrug resistance 2 Rat metabotropic glutamate receptor (GLUR4) mRNA, complete cds
24458 A		1711	NM_022706			
24501 D		1167	AI232006			Rattus norvegicus translation elongation factor 1-delta subunit mRNA, partial cds
24508 E		1416	M34643			Rat neurotrophin-3 (HDNF/NT-3) mRNA, complete cds
24577 A		1498	X55153			ESTs, Highly similar to RLA2 RAT 60S ACIDIC RIBOSOMAL PROTEIN P2 [R.norvegicus]
24589 E,P		1558	NM_012674		Serine protease inhibitor, kanzal type 1/ Trypsin inhibitor-like protein, pancreatic	Serine protease inhibitor, kanzal type 1/ Trypsin inhibitor-like protein, pancreatic
24597 C		1625	NM_017040		Protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	Protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform
24645 A		1484	V01225	Starch and sucrose metabolism	HMM:amylase 2, pancreatic	Rat pancreatic amylase mRNA, partial coding sequence
24651 P		1426	M83678			Sprague-Dawley (clone LRB10) RAB13 mRNA, 3'end
24654 E		100	AA819333			Sprague-Dawley (clone LRB2) RAB16 mRNA, complete cds
24670 G		1642	NM_017189		asialoglycoprotein receptor 2	asialoglycoprotein receptor 2
24707 E,O		1561	NM_012693	Fatty acid metabolism, Tryptophan metabolism	Cytochrome P450 IIA2	Cytochrome P450 IIA2
24710 C		1430	M98820	interact6-1	Interleukin 1 beta	Rat interleukin 1-beta mRNA, complete cds

TABLE 1				Document Number:160775		
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	UniGene Cluster Title
24721 Q		99	AA819306		Plasma kallikrein	ESTs
24722 G		1564	NM_012725		Solute carrier family 10 (sodium/bile acid cotransporter family), member 1	Solute carrier family 10 (sodium/bile acid cotransporter family), member 1
24771 A,G		1626	NM_017047	Cysteine metabolism, Glycine, serine and threonine metabolism, Oxidative phosphorylation		
24779 F		1375	J03863		Hs:serine dehydratase	Rat serine dehydratase (SDH2) mRNA, complete cds
24810 F,G		1391	L22339	Sulfur metabolism	sulfo transferase, phenol preferring 2	Rat N-hydroxy-2-acetylaminofluorene (ST1C1) mRNA, complete cds
24811 G		1391	L22339	Sulfur metabolism	sulfo transferase, phenol preferring 2	Rat N-hydroxy-2-acetylaminofluorene (ST1C1) mRNA, complete cds
24826 P		1421	M63991			Rat thyroxine-binding globulin (TBG) mRNA, 3' end
				Androgen and estrogen metabolism, Pentose and glucuronate interconversions, Porphyrin and chlorophyll metabolism, Starch and sucrose metabolism	Hsp-UDP-GLUCURONOSYLTRANSFERASE 2B1 PRECURSOR, MICROSOMAL carbonic anhydrase 5	Rat liver UDP-glucuronosyltransferase, phenobarbital-inducible form mRNA, complete cds
24860 K,S		1403	M13506	Nitrogen metabolism		
24883 A		1677	NM_019293			
25024 F		1353	E03229			
25052 A,F,M,P		1390	L22190			
25054 A		1396	L36460			
25055 K		1398	M11251			
25056 K,L		1402	M13234			
25069 F,G		1440	S82820			
25077 Q		1453	U20643			

TABLE 1					Document Number 1650775	
GLGC ID	Comparison Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
25083 P		1473	U72632			
25098 J		1	AA108277	Arginine and proline metabolism, Glycine, serine and threonine		
25183 K		495	AF050159	metabolism, Histidine metabolism, Phenylalanine metabolism, Tryptophan metabolism, Tyrosine metabolism, beta-Alanine metabolism	Hsp MEMBRANE COPPER AMINE OXIDASE	
25198 J		1689	NM_021754		insulin receptor substrate 2	
25203 E		501	AF079873			
25246 M		1321	AJ011607			
25257 C,I		1328	D13623			
25290 M,O		1339	D42148			
25313 I		1347	D87991			
25370 B,Q		1387	L16995			
25379 Q		1394	L26292			
25397 E		1401	M12822			
25409 E		1408	M18527			
25410 E		1409	M18528			
25411 E		1410	M18529			
25413 E		1411	M18531			
25480 A,G		1432	S46785			
25525 P		1437	S72505	Glutathione metabolism	Hsp GLUTATHIONE S-TRANSFERASE YC-1	
25567 A,J		1441	S85184			
25615 E		1466	U58466			

TABLE 1					Document Number 1650775	
GLGC Comparison ID	Code	Nucleotide Sequence ID	GenBank Acc ID	Pathways	Known Gene Name	Unigene Cluster Title
25618	M	1470	U64705			
25619	M	1470	U64705			
25632	G	1476	U75405			
25644	E	1479	U77931			
25675	A	1493	X14181			
25702	A	1502	X58465			
25705	H	1504	X59375			
25706	L	1506	X59608			
25718	I,O	1508	X62145			
25725	K	1510	X62660			
25747	A,F	1518	X81448			
25768	Q	1520	X94769			
25777	E	1523	Y08355			
25802	E,I	1352	E02315			
25814	H	1696	NM_022268			
25852	L	1305	A1639898			
25892	G	1309	A1639101			
25907	J	1313	A1639167			
25938	B	1314	A1639281			
26088	E	291	AA901152			
26109	S	441	AA907009			
26123	D	511	A1008396			
26133	M	532	A1009950			
26147	E	563	A1013387			
26152	N	576	A1028938			
26190	E,R	688	A1072578			
26280	Q	1082	A1227562			
26288	E	1134	A1230577			
26320	M	1242	A1234927			

TABLE 1		Nucleotide Sequence		GenBank Acc ID		Pathways		Known Gene Name		Unigene Cluster Title		Document Number 1680775	
GLGC ID	Comparison Code												
26368	E	1367 H34047											
26369	C.D	1369 H34687											

TABLE 2		Document Number 1650775
Comparison	Comparison Code	
General Toxicity: Amitriptyline, ANIT, APAP, CCl4, Diclofenac, Indomethacin, Valproate, Untreated Rats, Various Vehicles, WY-14643, Cyproterone Acetate, and Estradiol	A	
Hepatitis-inducing and NSAIDs: Diclofenac and Indomethacin	B	
Necrosis and Fatty Liver: Carbon Tetrachloride and Valproate	C	
Necrosis With and Without Fatty Liver: Carbon Tetrachloride, Valproate, and Acetaminophen	D	
Protein Adduct Formers: Valproate and Diclofenac	E	
ANIT	F	
Late Acetaminophen	G	
Early Acetaminophen	H	
Late Carbon Tetrachloride	I	
Early Carbon Tetrachloride	J	
Late Cyproterone Acetate	K	
Early Cyproterone Acetate	L	
Late Diclofenac	M	
Early Diclofenac	N	
Estradiol	O	
Late Indomethacin	P	
Early Indomethacin	Q	
Valproate	R	
WY-14643	S	

0917800 073101

TABLE 3A: General Toxicity				Document Number 1650775	
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
21471	30.43	93.54	75	-42.67	24.83
13203	35.33	61.64	74	-31.14	29.79
19909	22.08	33.51	73	-15.41	29.38
4553	13.83	18.08	72	1.43	6.49
15301	124.27	140.5	77	5.51	36.16
20456	42.5	31.85	70	7.46	20.45
23679	57.12	66.55	72	8.07	7.49
14693	37.57	38.27	72	9.49	11.63
12471	26.73	25.33	73	9.55	21.73
923	60.74	80.74	71	9.6	6.57
15647	49.51	40.73	72	10.9	23.58
6322	45.84	55.48	70	12.42	10.76
16314	48.7	48.51	70	12.45	16.75
25052	90.08	154.89	70	14.05	18.5
2164	57.65	53.74	73	14.96	17.31
16006	58.93	36.27	80	15.18	19.39
25054	45.65	42.59	72	15.37	40.01
6410	4.65	23.5	70	15.8	61.49
23500	39.03	35.28	70	16.65	11.6
16312	39.06	24.35	75	17.24	10.59
19843	2.55	18.74	74	17.7	10.31
14996	58.1	47.71	71	20.43	22.52
16085	60.79	45.9	70	21.59	14.6
17982	49.3	27.48	70	23.22	18.41
6226	46.81	36.97	71	23.54	10.28
9326	6.05	16.52	70	24.18	25.4
15055	-7.1	34.32	70	24.3	26.9
351	94.58	92.7	71	26.37	19.43
1126	48.74	21.68	72	26.96	14.06
20161	87.17	88.37	76	27.44	26.92
8766	-14.3	48.76	75	27.97	35.81
23511	12.84	20.12	72	29.05	16
5461	77.51	74.15	71	29.28	16.66
12216	-22.58	61.28	71	29.83	80.65
5384	100.6	91.07	76	30.03	29.52
18389	43.98	46.66	74	31.53	26.82
21695	45.44	55.44	72	31.53	16.62
11357	17.28	18.76	73	31.76	16.7
14424	567.82	812.48	70	32.4	34.02
9331	60.44	27.33	70	33.81	15.06
23767	23.85	17.49	71	34.2	50.3
15862	62.08	31.33	71	34.72	12.31
20449	117.61	143.09	71	35.82	9.2
10248	68.54	26.33	77	36.88	16.24

TABLE 3A: General Toxicity				Document Number 1650775	
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
23082	23.23	17.75	71	37.04	12.65
9425	17.36	27.44	71	37.87	17.12
16730	73.58	39.38	73	39.09	20.24
9583	161.94	162.1	73	39.37	25.85
11563	71.92	56.8	70	39.98	27.02
352	130.52	119.67	76	40.04	18.99
6604	24.19	16.7	74	41.3	15.53
7243	91.87	50.42	74	41.4	14.59
17709	71.49	47.04	70	41.77	28.89
1583	62.93	26.33	71	41.81	9.01
761	28.63	19.45	70	43.38	21.32
3849	81.84	39.76	71	43.61	16.59
24284	65.8	20.86	74	45.29	13.2
3207	25.59	109.41	70	45.31	54.06
21707	108.81	66.66	72	45.32	39.4
17589	85.64	50.71	71	46.93	27.53
22212	112.59	77.44	70	47.96	21.25
5175	72.78	115.19	71	48.48	31.56
7299	220.49	225.32	77	49.33	34.75
19678	3.58	46.62	75	49.59	34.93
21088	58.85	18.82	72	51.63	11.12
15892	152	118.78	75	52.52	42.58
14353	84.25	29.24	74	53.47	12.39
11527	119.25	79.46	70	54.98	27.79
13749	38.3	29.23	73	55.43	20.89
4281	38.95	21.16	70	57.15	17.8
353	194.24	177.12	76	57.46	26.37
14206	41.14	16.67	73	57.71	14.34
16080	207.65	183.99	77	58.82	28.68
6682	53.78	37.44	70	59.02	19.46
825	42.12	20.91	71	59.35	17.09
7918	90.4	45.57	71	60.65	23.06
21150	138.34	101.42	71	64.19	46.67
7531	57.13	26.96	70	64.99	18.47
22487	81.97	69.8	71	66.94	27.76
24264	112.04	51.05	72	67.41	29.12
22077	46.19	26.57	70	67.77	24.16
21209	174.43	157.48	73	70.46	46.49
20772	102.74	37.31	72	70.49	15.59
8600	33.46	36.07	72	71.84	38.68
9826	49.36	28.75	70	72	22.77
17688	108.65	39.15	70	72.62	19.69
8640	40.46	39.18	74	73.64	29.52
3074	75.98	91.66	70	73.84	44.71

TABLE 3A: General Toxicity				Document Number 1650775	
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
4473	54.98	25.48	70	74.37	21.06
354	227.5	203.23	77	74.89	23.89
23522	107.75	42.24	73	74.91	18.29
15299	176.87	143.39	75	75.35	20.66
13166	145.19	92.31	71	75.39	33.67
7936	59.06	21.73	70	76.33	18.71
17819	57.46	25.12	71	76.84	20.15
17908	191.58	159.91	71	77.06	30.42
7681	125.85	57.35	71	77.88	39.68
23633	66.31	40.72	70	78.12	28.98
19508	49.65	31.49	70	78.53	32.19
9541	166.47	123.33	72	79.59	34.68
16446	58.49	21.61	71	80.2	20.86
17377	119.83	80.06	72	82.65	37.63
20801	136.04	60.94	71	83	38.58
7352	164.48	94.53	70	83.91	38.34
2901	63.21	31.06	71	84.9	24.78
15156	85.12	43.67	71	85.31	23.45
22877	140.94	62.91	71	85.66	25.88
15207	112.17	89.27	73	85.8	32.15
9627	65.98	37.05	73	86.7	25.5
4017	71.08	40.29	70	86.72	27.99
4944	252.32	217.46	76	86.84	38.34
3073	78.22	126.03	72	87.19	58.64
5046	99.33	75.05	70	91.34	37.3
3713	66.05	38.37	71	91.52	27.81
11576	56.54	27.2	75	92.19	28.07
1246	57.52	28.55	70	92.34	25.09
15382	699.61	884.63	73	92.89	30.78
18109	105.09	108.04	71	93.58	44.98
18906	66.76	34.6	72	93.87	22.06
16324	65.53	39.09	72	94.25	27.97
7903	31.76	35.55	72	94.94	65.97
7063	179.3	93.83	74	95.16	22.48
9053	60.23	42.49	72	97.12	25.77
5813	67.41	28.11	70	97.48	35.73
9245	39.62	45.11	73	97.55	55.74
16081	293.48	225.5	78	97.81	34.89
19085	146.97	54.5	71	98.39	27.86
3189	48.18	30.77	70	99.15	55.31
12655	74.53	78.23	70	99.85	45.15
5219	54.76	44.93	70	100.79	47.29
7062	157.19	68.98	70	101.14	24.11
6820	132.9	40.9	71	101.15	18.57

TABLE 3A: General Toxicity				Document Number 1650775	
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
21025	52.78	49.73	75	102	38.88
14746	72.12	42.89	70	102.6	35.3
11745	127.84	29.61	71	102.7	19.78
20035	330.62	323.46	73	105.65	47.24
12587	72.78	43.64	72	105.95	35.48
2372	89.09	42.56	70	107.07	30.91
2383	87.59	39.36	72	108.56	32.43
2532	28.55	57.57	72	109.2	73.94
11959	91.5	26.27	70	109.84	20.36
24375	200.33	108.66	72	110.42	32.85
15884	135.81	86.11	70	111.91	36.88
2576	81.51	44.81	71	112.47	36.08
23955	98.48	60.26	72	113.59	36.89
5008	152.54	61.16	71	113.65	24.98
20891	174.25	85.84	72	114.45	35.06
18390	78.44	44.36	70	116.93	42.8
1844	172.33	73.68	70	117.06	23.94
17591	177.66	76.44	70	119.35	26.88
22038	178.88	77.12	70	119.93	32.92
20874	102.83	26.99	76	120.76	19.57
17844	225.91	107.09	73	120.8	50.32
11691	80.29	49.49	73	124.21	42.81
19086	192.42	71.46	72	124.7	32.65
14937	93.31	50.67	75	125.88	34.64
20513	76.12	59.17	72	127.29	74
6037	90.3	39.56	73	127.31	44.99
12332	24.75	72.13	73	128.95	100.98
17335	99.84	36.82	73	129.97	30.57
134	71.14	58.38	77	133.41	39.47
7784	109.76	36.32	70	134.08	25.84
25567	222.63	133.25	70	134.17	40.36
4951	296.48	152.65	74	135.21	102.87
13351	87.72	56.78	76	135.45	45.49
22432	207.69	93.56	71	137.45	35.3
3075	134.78	146.57	74	138.67	65.46
16134	88.41	44.61	74	139.59	36.27
18660	99.04	62.72	74	141.07	60.13
17225	208.62	72.16	71	141.32	36.37
10509	91.25	50	70	142.42	48.95
6190	108.44	39.25	71	142.68	30.93
17393	216.6	101.01	70	144.48	27.96
22197	295.18	157.65	75	144.6	54.77
19952	98.31	43.39	75	145.63	36.13
1690	206.44	90.45	70	147.21	36.46

TABLE 3A: General Toxicity				Document Number 1650775	
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
23044	188.12	53.18	74	148	23.7
22931	50.06	64.25	72	148.05	101.64
14776	103.46	45.74	74	148.29	40.54
14051	218.89	97.53	70	149.85	36.11
22569	103.93	53.65	76	150.14	42.57
11403	485.69	353.08	74	150.23	94.34
13762	105.01	72.99	71	151.26	47.6
14074	72.32	60.1	74	153.35	74.91
18960	120.13	59.4	71	156.6	44.43
20889	193.77	86.18	70	156.83	37.64
4084	127.09	64.08	71	158.37	49.57
18854	124.79	56.31	70	158.52	38.36
20735	294.63	147.51	80	164.19	33.2
14181	117.28	41.72	73	165.97	41.05
24883	122.66	51.37	75	165.99	38.66
15933	192.2	65.93	70	166.13	35.32
18792	112.37	55.57	73	167.2	48.33
10544	240.01	60.23	77	167.22	32.41
14208	98.76	46.96	77	167.76	48.04
20734	292.65	126.84	78	169.42	39.52
17334	283.45	131.16	76	170.46	50.64
22457	319.78	159.2	71	170.89	83.07
21978	127.23	34.44	75	172	37.41
20088	138.87	33.78	75	173.08	29.79
15300	301.38	143.25	73	174	53.02
16364	109.25	72.42	74	174.33	56.68
8829	280.85	107.19	74	174.35	39.95
1007	71.78	95.85	73	174.52	94.52
6443	130.76	76.39	77	174.54	46.87
17154	237.49	69.3	73	174.79	36.28
6473	107.85	42.8	72	175.56	60.84
2335	121.97	52.51	71	175.91	56.34
12450	90.03	92.4	75	181.36	63.89
16700	116.46	131.83	75	181.51	86.73
15955	105.87	86.17	73	183.02	74.51
23523	254.3	77.51	75	184.72	39.26
15900	300.11	139.69	72	184.95	58.44
10545	272.15	72.91	74	188.26	35.42
16982	503.02	283.02	72	188.67	203.36
12848	147.36	47.97	70	188.99	42.1
5749	219.23	62.17	70	189.76	42.51
15004	289.65	146.93	71	189.87	51.07
23075	307.83	118.82	72	190.09	58.23
23584	123.89	91.92	73	190.24	73.31

TABLE 3A: General Toxicity				Document Number 1650775	
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
14997	311.34	155.46	77	193.29	31.96
7617	133.32	123.53	70	193.38	108.54
11404	425.93	237.07	74	193.8	75.57
14095	145.71	64.97	77	194.48	44.06
16766	128.68	62.34	72	197.3	64.57
13757	132.12	63.33	72	197.76	47.88
3981	165.72	126.27	71	199.27	79.29
6632	374.92	164.24	76	199.58	56.28
22770	344.97	196.08	74	199.66	52.17
1099	159.6	51.35	71	200.56	47.88
15170	132.07	62.08	79	201.16	44.18
21125	104.89	85.5	74	205.52	74.23
23499	149	73.65	71	206.76	68.16
16765	131.63	64.51	74	208.95	60.5
23321	173.83	57.63	71	209.49	31.61
18908	94.04	112.32	72	209.75	126.49
4360	159.27	76.32	72	212.18	102.53
5027	165.48	78.52	73	212.59	52.82
14007	147.14	73.93	77	213.84	62.97
4719	153.89	88.13	74	216.28	70.99
9754	78.35	97.33	75	218.88	111.68
5867	342.61	167.79	70	219.32	57.15
16859	374.28	189.12	73	220.43	60.14
24434	132.32	69.32	71	226.73	56.25
22683	206.07	65.39	71	228.15	41.78
13963	218.82	179.67	72	228.18	75.69
11179	165.79	72.22	70	230.16	61.5
23445	110.29	87.9	82	231.61	62.42
18115	174.03	108.43	71	231.75	102.05
11429	189.45	42.84	72	232.42	40.03
11520	175.16	127.89	72	233.8	92.23
7927	202.04	106.05	70	234.79	57.37
22099	137.03	97.01	71	235.76	97.02
7888	376.09	171.23	72	236.43	56.75
17496	75.49	73.53	76	239.51	173.47
11742	161.82	79.25	71	239.68	82.64
6855	194.24	59.54	71	245.57	58.27
22928	87.17	110.53	70	245.88	162.18
7064	397.22	140.47	77	247.28	40.15
10879	202.31	103.86	70	248.56	66.82
20757	401.81	200.88	71	249.74	57.1
7113	200.31	111.11	74	250.23	78.75
11635	186.84	60.17	75	254.75	47.63
135	174.94	73.25	78	256.19	65.78

TABLE 3A: General Toxicity				Document Number 1650775	
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
24235	390.14	159.67	70	259.52	50.47
1479	205.28	61.98	72	261.61	51.03
5923	172.52	80.09	78	262.06	70.65
15642	368.73	123.22	77	262.87	41.31
9336	140.36	75.51	72	264.38	147.6
23325	326.83	125.56	70	265.55	63.28
9063	214.94	71.54	74	266.92	47.88
23612	382.82	255.62	72	267.25	92.93
912	326.5	67.38	73	268	33.47
14506	208.78	65.03	70	272.49	69.62
5748	328.41	66.67	70	274.63	44.97
8477	399.36	174.12	71	275.64	90.8
11021	177.75	93.53	73	275.95	97.97
8630	206.38	87.63	72	276.18	71.7
12331	142.97	91.35	73	276.42	113.01
12694	196.38	106.12	70	280.6	91.59
23380	201.35	91.04	71	280.63	98.56
25747	406.23	174.62	79	281.96	48.12
3418	416.76	178.28	75	282.48	51.77
19298	475.37	243.42	71	283.29	78.74
23558	187.58	94.53	72	284.57	75.57
6366	365.38	251.12	70	289.81	76.83
14103	153.89	84.24	76	291.22	113.41
24219	410.88	138.62	75	297.66	69
1929	232.96	81.98	71	298.56	77.17
5863	225.48	130.42	75	299.73	84.35
3504	395.85	157.69	70	301.1	58.36
4868	220.65	100.78	75	301.7	70.8
1753	235.94	62.13	72	304.05	74.62
22679	185.35	110.73	72	304.26	119.66
23230	431.68	274.8	77	305.51	73.66
17401	211.41	101.33	70	308.15	101.7
4179	444.58	228.79	73	308.58	63.03
24645	228.44	65.97	73	308.66	90.32
19679	212.7	94.25	74	309.08	79.13
8387	209.62	77.78	74	309.81	64.43
17324	236.31	65.13	73	311.13	52.23
1501	434.85	171.45	79	314.29	63.39
22582	224.5	87.58	71	316.36	75.3
25702	423.41	113.7	72	320.39	51.32
9399	222.67	63.69	76	320.67	86.48
3131	228.57	86.2	72	321.25	92.07
812	231.65	67.37	76	321.96	51.58
15519	303.98	284.36	71	322.04	142.67

TABLE 3A: General Toxicity				Document Number 1650775	
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non-Tox Mean	Non-Tox Stdev
1409	258.93	68.93	72	323.5	60.85
17049	207.81	93.01	77	324.1	63.71
7003	213.89	133.94	75	328.74	101.01
15612	208.41	106.4	71	329.06	202.57
851	259.03	53.32	76	331.68	47.82
4291	203.94	139.04	77	334.29	127.4
1478	262.27	68.1	74	334.41	51.89
7868	201.78	131.72	80	338.05	94.52
19469	284.04	59.16	72	342.98	50.36
15700	259.03	65.96	77	345.34	50.31
15197	263	83.78	70	348.89	85.31
2484	152.64	144.08	75	349.45	189.22
21396	274.52	76.97	73	354.24	57.86
15032	262.98	104.76	72	354.96	94.2
6825	321.55	146.79	71	355.67	98.41
14767	212.27	97.6	80	359.19	95.6
15136	482.9	133.86	71	361.06	68.44
2993	498.11	173.18	73	362.5	53.1
1175	211.25	155.83	72	367.03	107.25
16680	296.57	157.31	71	368.4	135.7
961	300.69	83.8	73	370.86	65.28
2696	463.19	111.26	71	371.94	59.78
17256	266.11	96.28	72	373.05	70.36
4937	305.59	112.68	74	375.59	89.26
18860	314.98	128.88	70	375.92	92.09
23884	312.54	72.12	70	379.68	59.35
17850	516.17	220.77	70	383.69	72.82
17175	504.94	132.64	72	384.43	64.15
12946	275.06	103.13	74	384.61	80.84
23322	308.64	91.46	73	385.69	58.02
16327	318.14	112.83	72	386.27	63.57
6824	820.68	540.91	70	386.87	102.09
1900	230.35	153.17	72	387.22	135.44
14869	290.26	114.01	70	388.39	93.33
15239	472.89	104.14	70	393.48	56.96
20694	256	155.8	75	396.34	127.36
6321	661.68	352.96	71	397.84	101.24
21157	628.44	255.63	70	401.01	132.71
1529	316.33	75.8	73	401.61	56.86
5934	166.87	133.41	76	401.67	162.84
18597	452.56	154.66	72	402.92	64.14
6801	284.93	123.62	70	403.58	114.82
8317	302.02	115.59	71	403.7	92.47
3959	651.41	284.48	73	404.94	125.39

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TABLE 3A: General Toxicity				Document Number 1650775	
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
6017	218.37	162.51	71	408.35	157.64
7785	309.16	154.16	71	411.11	92.69
18453	272.77	135.91	72	412.12	103.91
11157	347.22	111.72	73	412.71	76.32
2799	186.49	165.24	73	413.66	193.94
18606	551.54	140.45	71	415.6	65.98
25480	298.56	93.25	80	417.76	62.1
6554	327.78	86.42	75	418.15	72.16
22395	337.48	106	70	424.15	101.1
18861	353.52	146.94	71	431.18	96.34
556	363.95	72.87	72	431.39	47.74
15016	614.84	191.45	72	431.42	106
20707	297.52	182.87	72	432.6	110.59
6615	313.91	151.88	70	435.29	105.91
25675	559.03	149.18	71	435.84	78.46
24458	391.59	66.22	70	440.47	58.22
2264	348.28	114.55	70	442.01	101.65
811	339.77	83.76	80	442.46	54.75
14962	595.24	186.44	71	443.26	86.3
9905	351.99	86.2	73	443.66	62.13
4670	1011.12	757.17	70	449.34	279.51
15135	572.07	128.52	72	452.98	71.41
1877	381.72	99.89	72	455.58	70.01
2905	368.76	236.61	74	455.99	171.06
10176	362.61	131.62	73	458.21	78.68
8880	270.36	150.83	71	461.94	178.82
21977	333.82	102.68	78	464.63	71.57
19103	373.87	152.27	72	466.17	87.18
2505	361.86	109.11	73	466.31	72.15
7582	256.38	164.17	72	466.34	223.76
18001	369.81	89.98	72	467.77	75.36
15755	405.73	112.28	71	473.79	67.48
24577	583.7	137.54	73	474.11	65.9
20299	326.39	113.27	76	477.33	90.93
7697	273.75	100.92	83	481.09	117.81
18867	425.79	164.92	71	486.56	85.09
16726	386.57	78.35	71	489.29	90.61
18522	338.66	110.39	78	493.05	127.44
794	364.93	131.6	73	493.86	73.31
21097	596.6	213.78	72	494.87	76.63
11166	392.77	163.68	74	496.16	102.35
3823	819.94	253.21	84	496.62	131.46
20701	546.93	267.9	71	497.17	122.04
13283	374.45	137.36	71	498.65	90.97

TABLE 3A: General Toxicity				Document Number 1650775	
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non Tox Mean	Non Tox Stdev
14312	379.02	130.24	70	498.8	162.03
1561	489.56	192.41	70	503.1	74.48
11693	280.1	210.45	74	504.39	202.02
19470	355.43	120.62	75	507.23	102.75
20705	406.75	228.32	72	520.73	125.68
6060	377.46	110.54	75	524.04	95.02
4143	411.36	153.04	70	526.83	142.72
573	397.93	141.77	74	527.31	101.53
2111	431.14	135.97	70	535.18	95.74
6132	389.97	132.3	70	536.05	116.38
1531	432.89	99.85	74	537.37	84.23
13684	732.21	234.57	71	538.64	123.03
4914	320.44	176.4	77	542.57	159.28
16172	384.09	149.87	71	543.43	107
18661	375.83	155.78	71	546.25	136.03
14035	354.4	185.79	72	546.44	215.25
18452	376.32	156.49	75	548.91	124.57
10109	683.1	154.88	71	554.69	60.26
15113	422.52	185.06	72	557.21	136.1
12087	426.39	140.52	70	558.91	91.57
11492	398.17	152.29	73	559.08	143.79
14083	400.42	184.48	74	569.39	131.38
23961	487.24	102.51	71	571.23	72.66
6761	734.58	239.42	73	572.66	144.55
16993	402.56	131.25	80	574.27	86.25
11536	347.49	123.19	77	575.39	198.99
12312	415.93	131.04	75	579.26	98.18
20810	686.37	181.4	70	589.89	79.84
24771	441.44	127.76	75	592.18	94.5
6007	477.65	139.01	76	592.68	113.45
3145	432.3	212.79	72	610.87	178.16
12064	392.31	195.73	78	611.49	148.58
15080	468.83	133	74	613.82	131.38
22338	858.3	334.36	70	633.42	176.07
23437	417.21	173.85	75	633.59	238.89
20397	775.65	145.47	74	638.29	86.47
22930	206.34	282.8	72	638.83	389.14
5943	365.28	277.04	78	658.15	266.99
13088	440.35	191.07	72	659.11	130.73
3969	461.16	167.2	73	671.43	138.26
2536	229.18	164.07	75	680.76	402.5
8946	488.94	198.29	74	698.4	191.02
1173	454.86	255.52	73	701.71	147.85
6613	475.14	319.24	71	703.21	206.38

TABLE 3A: General Toxicity				Document Number 1650775	
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non-Tox Mean	Non-Tox Stdev
17847	587.34	146.42	73	728.57	116.89
19069	401.65	251.38	70	736.55	312.13
3121	582.17	314.22	75	743.82	177.43
2762	549.37	222.1	73	744.04	144.72
9191	353.85	236.51	80	747.6	226.01
17339	394.82	309.4	71	757.04	450.78
3365	465.6	196.26	75	759.09	201.02
5622	781.85	245.85	70	761.19	118.25
19729	390.13	332.32	78	764.27	355.89
9012	363.63	210.98	77	764.48	253.76
4193	592.69	173.22	72	771.85	108.77
8549	428.57	212.41	77	776.74	195.59
16190	633.77	300.61	71	788.33	198.05
6143	563.65	311.9	76	807.95	145.12
11228	611.37	254.64	71	817.25	249.82
19830	639.79	218.85	75	827.94	161.07
11504	659.77	278.75	70	831.93	222.74
2569	457.34	317.75	82	855.43	152.77
12160	812.82	573.26	70	864.88	230.19
21341	583.63	407.72	73	869.75	255.69
24321	471.3	256.45	83	871.6	204.88
14584	778.69	204.76	72	899.51	154.36
4440	592.51	190.31	81	903.2	141.99
17340	1192.58	780.31	70	918.51	258.08
2196	676.58	230.37	76	961.23	265.77
16879	875.19	424.83	74	998.63	195.4
14118	716.41	266.36	72	1006.89	263.75
20503	598.26	362.91	74	1021.64	320.28
12306	1122.58	844.77	71	1023.1	338.53
2911	675.36	278.69	72	1039.76	290.7
18796	825.55	557.51	70	1043.22	369.63
19732	639.42	377.16	74	1044.68	344.85
11205	763.23	299.36	72	1062.45	233.92
13634	1541.83	591.67	70	1065.68	230.26
8692	729.45	328.96	71	1075.69	284.09
22559	707.2	351.3	74	1078.43	298.05
9475	633.07	305.29	76	1091.11	321.49
6033	695.09	293.08	78	1093.71	230.15
7893	681.36	341.8	72	1123.77	299.15
3822	1790.91	546.55	78	1156.91	279.92
18910	691.91	316.7	77	1158.26	375.48
16703	811.27	347.36	78	1176.58	244.51
10984	769.03	347.66	74	1177.95	295.11
24162	935.19	218.55	71	1183.5	254.36

TABLE 3A: General Toxicity				Document Number 1650775	
GLGC ID	Tox Mean	Tox Stdev	LDA Score	Non-Tox Mean	Non-Tox Stdev
14960	1815.81	619.16	72	1189.85	282.97
22368	809.54	304.72	78	1204.44	255.44
14512	758.14	344.89	75	1207.73	316.98
22929	345.04	524.79	76	1263.79	749.31
6633	1158.38	523.64	70	1282.41	230.42
5899	868.41	419.97	75	1320.55	275.91
17027	885.56	416.43	74	1334.54	460.45
633	1120.93	302.27	71	1460.55	215.38
15240	1096.17	411.07	71	1507.99	426.62
3916	981.26	439.68	78	1583.55	340.89
22554	987.76	444.02	77	1595.12	393.47
3995	1025.02	387.98	75	1611.33	356.12
16885	1112.24	354.14	71	1613.71	341.53
9889	981.18	477.47	73	1620.07	396.24
15029	925.54	487.41	79	1688.81	378.2
6015	1123.82	384.91	78	1698.32	346
4330	991.16	483.62	84	1718.02	326.97
18909	1097.68	570.79	73	1735.42	607.51
3934	1109.15	552.14	74	1739.43	460.08
19363	867.12	620.13	74	1779.39	738.12
18002	1288.49	485.23	71	1800.22	448.73
4933	1364.86	630.42	74	1830.55	501.46
6380	1372.29	707.55	71	1841.36	514.23
16883	1363.62	527.7	78	2010.57	420.12
6072	1574.16	580.37	71	2013.52	377.64
17812	1417.56	569.56	70	2054.51	507.28
16701	1417.08	583.17	75	2071.93	447.2
6016	1345.93	620.12	75	2194.85	585.99
23261	1440.1	757.17	76	2245.13	579.05
9016	1484.15	791.38	72	2570.48	765.58
17524	1867.91	789.56	72	2578.07	684.86
22558	2228.15	660.37	73	3099.17	679.05
20502	2254.47	1019.37	72	3293.47	799.82

TABLE 3B: Hepatitis-inducing and NSAIDS				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
1661	41.81	18.92	85%	1.48	29.99
16317	30.67	11.58	80%	8.6	15.46
11893	54.33	34.89	85%	10.78	84.99
1507	46.98	9	89%	15.22	15.58
22966	36.69	8.83	81%	19.74	17.28
19671	37.69	7.44	85%	22.27	14.65
20016	36	8.96	81%	22.47	17.54
18495	49.47	12.55	87%	26.89	16.39
671	1.28	14.77	83%	29.18	22.7
1221	443.26	150.05	94%	31.23	89.26
25938	56.45	7.66	83%	32.22	17.92
18389	86.77	18.28	87%	33.41	32.92
11974	-0.81	15.18	84%	37.19	30.74
15834	-27.94	45.21	80%	40.53	65.46
20161	128.51	48.18	89%	43.77	57.9
17809	73.73	16.32	83%	46.32	27.65
7056	3.07	13.95	81%	47.6	27.96
5384	140.18	41.23	89%	47.78	62.23
16809	124.52	30.87	89%	53.12	26.62
11423	97.3	21.17	90%	54.32	20.04
22918	25.37	5.71	92%	57.72	29.27
20354	223.3	84.74	94%	65.21	49.13
18529	131.4	33.67	86%	68.42	53.24
1514	90.15	14.51	83%	70.26	23.25
8079	-4.51	23.75	93%	71.3	43.24
23847	116.7	16.84	84%	72.04	35.87
9712	23.03	12.25	88%	77.04	28.42
3660	16.83	21.57	82%	79.66	62.38
11904	167.34	25.7	93%	81.27	36.83
19158	45.35	20.66	81%	83.61	36.03
3710	-36.33	22.78	94%	85.53	112.55
15207	201.4	59.51	87%	87.46	53.13
18272	60.07	14.42	82%	88.02	33.03
353	141.35	40.91	85%	91.87	108.42
19410	151.13	23.55	87%	95.16	23.41
22321	170.96	42.18	92%	100.6	89.13
17277	197.62	54.02	87%	107.61	40.04
6597	164.65	22.23	88%	114.16	40.18
22151	53.9	21.51	85%	114.65	59.1
8274	76.86	17.29	87%	123.17	47.02
6532	271.93	51.51	94%	134.9	41.19
21570	190.77	30.4	81%	139.02	39.64
2555	331.4	107.66	92%	140.78	56.13
25370	84.18	22.52	80%	142.29	76.05

TABLE 3B: Hepatitis-Inducing and NSAIDS				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
14208	94.74	20.59	84%	147.42	57.13
4250	206.6	31.57	81%	151.25	44.71
1521	259.23	49.47	85%	156.72	61.63
19075	223.09	35.39	81%	163.86	101.01
23584	77.34	44.36	81%	169.97	88.21
23855	348.59	60.39	85%	174.64	78.04
9595	340.35	75.95	82%	175.69	67.44
13332	103.75	23.14	88%	187.8	61.54
10544	215.74	17.73	83%	188.96	55.01
20914	95.15	42	80%	195.52	132.48
1796	121.33	29.79	82%	209	97.51
21039	106.61	32.3	84%	211.38	102.32
18891	79.72	50.3	84%	246.65	190.37
5464	135.66	32.82	82%	247.44	149.05
15786	143.55	47.13	84%	247.54	88.85
22619	538.26	124.75	87%	252.1	119.33
2655	82.89	32.9	90%	258.6	179.08
12156	181.92	29.95	83%	278.7	159.97
17664	741.68	141.39	92%	307.07	186.68
3504	500.63	92.33	90%	315.63	104.18
21281	205.42	64.7	81%	330.89	91.63
23890	215.59	58.3	82%	335.94	112.79
21663	239	51.32	81%	340.75	88.67
1795	160.6	58.49	90%	341.81	148.58
6825	186.43	50.61	90%	343.11	120.89
1900	172.64	60.15	81%	346.3	165.46
18465	620.04	89.19	89%	351.76	235.3
19412	785.76	148.65	93%	362.14	121.09
4026	890.4	293.19	94%	365.48	125.1
9148	247.98	44.83	82%	370.2	91.6
12928	537.35	88.04	83%	411.28	98.02
2905	272.3	68.62	83%	428.13	203.06
21657	770.91	200.72	85%	465.93	129.71
15127	328.43	46.16	84%	473.84	141.3
20701	957.82	322.59	85%	491.66	156.52
23125	211.15	54.99	87%	522.67	517.03
15606	391.12	82.13	80%	555.3	143.44
13557	380.72	110.05	84%	601.18	180.33
3365	412.07	116.59	83%	652.4	245.48
18890	249.81	125.41	88%	681.61	362.92
21740	1634.89	574.14	94%	692.6	269.8
3121	283.35	133.91	89%	701.53	256.63
16458	914	77.34	87%	721.93	196.36
11720	1413.34	300.55	94%	727.31	251.26

TABLE 3B: Hepatitis-inducing and NSAIDS				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
11504	489.83	118.52	82%	806.57	268.81
17768	607.41	128.96	82%	831.34	168.24
13093	311.95	133.36	85%	873.19	562.27
6236	496.56	151.3	84%	902.06	432.96
23449	168.69	130.37	84%	927.26	659.99
23989	1753.97	311.2	89%	1058.6	400.01
23448	180.53	167.78	84%	1073.75	757.46
24289	653.83	137.29	88%	1100.08	340.79
16885	781.13	224.04	92%	1490.2	403.55
3917	948.73	233.94	87%	1606.37	494.39
6072	1216.55	290.18	86%	1863.45	506.08
9016	1131.05	452.13	84%	2271.36	942.23
6189	1001.77	624.81	84%	2994.32	1665.75
16884	1730.22	430.96	83%	3305.32	4446.34

TABLE 3C: Necrosis and Fatty Liver				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
7271	47.32	123.63	82%	-98.96	40.35
1727	109.71	134.11	80%	-50.93	105.7
5780	186.95	173.5	86%	-46.09	31.81
13203	59.69	60.36	82%	-17.7	44.77
16513	26.79	31.17	82%	-17.26	20.41
14619	43.31	34.51	85%	2.15	12.76
4553	26.34	19.46	83%	3.22	9.94
13458	45.73	26.41	89%	5.65	18.85
1610	44.15	19.04	83%	12.68	16.79
14693	74.3	48.25	83%	13.17	17.15
23679	133.75	76.1	90%	13.54	19.85
20456	59.55	30.52	86%	15.2	27.25
5733	152.59	121.24	80%	16.96	49.09
23435	130.84	87.29	81%	21.19	45.23
15312	97.29	57.4	83%	23.69	24.18
23678	101.95	55.99	89%	23.69	13.19
15861	71.17	46.83	82%	24.47	42.1
9181	83.64	43.77	86%	24.64	15.48
1598	201.08	146.9	80%	25.42	45.83
19940	83.79	44.07	83%	25.73	17.82
9796	72.8	40.14	82%	25.76	21.99
16085	106.34	47.32	89%	28.48	22.62
13467	155.47	95.96	86%	30.98	34.92
16618	94.85	58.13	80%	33.73	25.67
24710	86.03	43.14	83%	33.9	21
23260	157.52	100.81	83%	37.65	37.29
22876	70.57	22.75	82%	37.66	16.34
9331	80.05	31.38	80%	38.03	18.65
12614	139.71	71.97	88%	39.91	23.39
3280	81.33	28.39	81%	40.1	20.81
13874	88.42	37.45	84%	40.85	22.09
15862	84.57	34.63	80%	42.44	41.06
5926	80.04	27.03	83%	42.65	20.36
20449	254.92	200.63	82%	44.06	38.62
15313	148.78	79.95	82%	44.12	32.74
2897	110.58	50.4	86%	47.14	25.32
10549	203.78	148.01	82%	49.51	39.18
7243	132.31	62.02	80%	50.65	27.72
14939	115.22	49.92	83%	53.09	45.97
14242	118.61	49.19	85%	53.41	25.56
7161	136.07	72.13	81%	53.54	28.94
20708	91.32	26.75	86%	53.6	18.5
3831	104.66	45.67	83%	54.97	24.3
21707	135.19	53.83	81%	55.69	51.38

TABLE 3C: Necrosis and Fatty Liver				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
19264	117.33	44.24	83%	59.31	20.88
19150	109.31	32.72	86%	60.72	15.98
17687	99.1	21.62	85%	61.04	15.35
14462	156.22	62.83	84%	62.47	36.02
7036	131.87	57.57	81%	62.54	25.28
11527	177.9	80.35	84%	62.69	44.14
20082	124.7	51.02	84%	63.08	42.14
17736	432.83	313.35	81%	65.71	142.15
1841	136.63	50.08	81%	67.1	44.8
20523	102.48	38.3	83%	67.66	66.06
12965	169.8	78.23	83%	71.26	51.46
6085	208.53	104.4	83%	72.61	45.7
14458	330.83	217.41	83%	73.29	65.46
24236	184.01	75.75	85%	73.32	33.88
23160	176.55	75.81	83%	73.36	35.73
13251	323.03	180.5	84%	75.07	50.76
9784	153.22	64.68	82%	79.16	35.89
15398	239.17	147.09	84%	79.65	55.81
353	280.56	162.02	81%	80.59	90.86
20684	131.06	32.29	86%	86.62	20.64
14258	198.53	76.19	81%	87.06	38.11
22877	194.7	70.48	86%	93.61	36.71
1411	202.73	82.72	81%	98.83	39.17
11660	170.21	44.78	84%	99.62	34.3
23099	201.64	75.74	81%	104.62	41.86
23438	195.84	62.14	85%	104.93	43.18
17734	614.42	397.11	81%	110.47	174.81
7063	256.37	132.72	84%	114.31	69.93
1399	215.1	91.12	82%	116.84	76.67
5008	201.49	60.1	84%	118.38	36.13
11331	223.98	89.07	83%	120.5	40.92
25257	274.45	132.38	80%	121.28	48.13
16321	210.67	63.57	83%	124.13	43.97
20891	244.46	85.07	84%	125.01	52.71
2938	92.66	29.87	81%	127.24	29.13
22038	251.93	88.6	85%	127.34	44.31
17369	207.5	75.1	82%	129.13	60.27
5794	226.31	75.22	81%	130.44	40.81
5489	273.17	111.54	82%	136.39	59.55
20843	213.04	53.39	82%	136.57	33.06
2555	219.93	71.85	81%	139.38	59
15374	243.38	59.14	83%	141.32	44.16
24388	624.21	327.48	89%	143.82	68.72
22432	292.49	109.98	83%	146.05	50.66

TABLE 3C: Necrosis and Fatty Liver					Document Number 1650775
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
18418	239.91	82.99	83%	146.58	40.53
12999	347.57	138.68	83%	153.73	65.66
26369	308.75	109.91	81%	154.12	55.73
14051	299.77	104	82%	156.87	52.25
4592	257.24	62.73	86%	157.37	38.03
4952	684.4	441.82	80%	158.99	145.89
23184	332.9	137.24	81%	159.3	52.72
7887	338.64	115.83	86%	162.05	60.73
18755	279.19	80.05	83%	163.56	53.86
17735	512.06	294.56	82%	167.32	151.69
4781	344.83	111.41	85%	169.37	65.78
22197	414.63	204.11	83%	169.48	88.02
23855	282.27	93.29	80%	171.07	75.56
14224	333.11	104.73	83%	174.8	67.56
6796	410.28	172.66	86%	185.7	72.52
20735	408.72	201.02	82%	185.89	74.3
21696	297.51	89.84	81%	186.09	42.02
11561	362.43	142.46	82%	188.78	64.86
3203	308.57	101.34	81%	194.76	46.19
7414	535.61	335.02	83%	197.35	92.11
15900	420.93	177.15	81%	202.45	80.18
23299	835.51	456.01	87%	214.06	131.12
2615	386.6	100.97	86%	217.6	65.98
5867	511.55	202.2	82%	233.57	78.63
24597	382.02	100.07	86%	233.91	54.34
11404	578.06	245.72	83%	238.77	146.51
1460	401.14	112.53	84%	244.96	91.82
498	416.48	120.92	83%	249.32	96.83
16859	472.45	162.72	81%	251.02	122.56
7888	537.76	182.29	85%	257.15	89.71
16756	553.61	229.09	83%	281.56	137.56
7064	502.34	176.81	85%	282.57	116.55
3418	612.35	201.12	86%	297.77	79.32
21458	1369.61	969.19	80%	306.95	224.17
2818	499.79	119.08	85%	321.5	81.64
23120	466.17	110.7	82%	322.94	76.21
4179	559.24	157.01	86%	323.2	127.86
21672	477.65	79.51	85%	327.31	77.78
23229	626.51	235.94	81%	338.12	95.94
1501	526.15	137.21	81%	342.01	115.25
7785	234.09	120.53	83%	402.39	211.3
6824	1330.86	651	84%	457.47	265.81
14962	735.07	188.78	85%	460.88	120.76
13646	647.84	120.93	81%	469.35	113.75

TABLE 3C: Necrosis and Fatty Liver				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
11693	194.51	110.15	81%	475.41	349.8
6132	303.54	124.75	81%	496.77	136.48
7935	319.95	130.18	81%	539.48	150.81
4193	471.49	196.67	86%	732.69	138.33
2569	363.05	288.34	84%	741.53	276.55
6143	440.17	239.99	82%	761.21	219.76
20503	406.67	194.67	86%	913.12	368.79
16703	657.32	260.25	82%	1074.26	319.63
7403	747.37	603.65	82%	1275.15	420.96
7199	888.57	501.29	81%	1460.27	432.28
15029	731.54	467.45	85%	1526.56	513.26
4330	744.46	374.66	83%	1547.62	486.62
6380	907.19	397.41	84%	1723.63	601.93
16883	1078.56	580.73	82%	1877.14	516.54
6016	1048.32	457.34	84%	2002.18	710.82
23261	1133.22	790.5	81%	2083.71	702.84
9016	1179.45	473.8	81%	2319.89	929.08

TABLE 3D: Necrosis With or Without Fatty Liver				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
5780	149.44	174.82	83%	-46.61	31.66
14619	39.67	32.26	81%	1.81	12.49
5504	40.54	56.94	82%	4.45	12.06
13458	39.01	28.21	82%	5.58	18.92
15860	31.78	22.42	81%	6.3	24.49
14693	68.27	45.68	82%	12.72	16.78
23679	113.2	81.03	82%	13.37	19.88
15312	89.9	55.01	81%	23.16	23.77
15861	75.5	43.95	86%	23.4	41.45
9181	78.27	41.53	85%	24.18	14.99
16085	90.49	54.22	81%	28.58	22.73
13723	125.68	115.97	84%	29.26	45.67
23260	150.76	92.71	85%	36.36	35.87
9331	78.82	28.75	82%	37.48	18.21
12614	122.76	74.47	81%	39.76	23.36
13874	91.42	39.76	85%	39.87	20
15862	87.12	32.75	83%	41.59	40.71
2838	145.55	92.3	83%	42.77	33.6
15313	138.73	76.22	81%	43.33	32.1
2897	102.26	48.95	80%	46.84	25.34
10549	187.81	138.33	82%	48.44	38.17
14939	109.91	48.48	81%	52.56	45.94
14242	115.77	46.52	85%	52.64	24.7
17736	447.8	300.15	85%	58.86	128.94
19264	110.15	43.15	81%	59.01	20.79
14462	146.65	60.75	83%	61.81	35.78
15663	150.74	81.27	81%	61.88	28.94
13251	296.06	174.05	83%	73.46	48.79
6012	176.64	72.48	83%	84.55	40.71
22877	181.18	70.29	80%	93.15	36.67
1411	191.96	79.06	80%	98.12	38.82
11660	165	42.53	82%	98.96	34.06
17734	628.16	382.62	85%	101.62	156.16
6820	162.7	43.24	81%	105.26	24.87
1399	254.19	123.38	83%	112.16	66.1
7063	246.94	123.92	84%	112.9	69.1
24375	284.9	130.19	82%	122.22	50.94
22038	242.92	82.73	85%	126.16	43.47
15282	345.28	174.2	83%	133.39	77.83
20843	205.85	51.68	80%	135.98	32.8
11235	307.17	131.67	83%	138.32	42.12
15374	245.25	54.33	85%	139.6	42.14
8886	258.45	90.02	82%	140.07	40.87
24388	550.6	333.76	85%	142.43	67.72

TABLE 3D- Necrosis With or Without Fatty Liver				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
6039	298.35	118.74	82%	149.78	54.28
26369	303.77	102.86	83%	152.16	53.29
14051	288.38	98.7	81%	155.61	51.3
4592	241.58	65.95	80%	157.11	38.16
17735	549.36	298.48	85%	159	133.2
7887	321.75	114.32	83%	160.72	59.56
18755	284.26	77.14	85%	161.37	50.75
4781	337.58	103.44	85%	167.27	63.76
20735	413.37	184.38	86%	182.1	67.45
7414	505.45	309.7	84%	194.61	89.53
11403	734.85	335.38	87%	196.39	177.82
15900	425.49	161.92	84%	198.73	74.48
15543	413.52	162.64	83%	212.02	73.08
23445	63.7	78.02	82%	213.22	89.74
6911	135.77	67.21	81%	214.68	51.49
11404	616.53	242.57	86%	230.44	130.03
5867	485.57	189.97	84%	231.42	77.22
1460	416.34	113.77	87%	241.33	86.89
7888	525.74	174.65	87%	253.82	84.82
26123	592.58	263.62	81%	267.76	130.29
16756	536.74	209.62	86%	278.76	136.63
24235	489.44	179.4	82%	280.21	94.54
3418	575.64	197.63	85%	295.93	78.26
19298	630.43	229.07	82%	317.49	143.34
23120	479.07	107.1	84%	319.7	71.63
2818	482.71	116.97	82%	320.15	81.06
15700	230.09	67.32	81%	324.4	64.93
228	236.54	61.87	80%	334.29	69.66
15032	205.99	56.82	80%	339.35	104.9
13294	644.35	170.98	82%	387.09	129.3
20707	228.73	113.6	81%	399.4	144.8
20299	283.13	98.83	81%	438.73	122.19
6824	1346.97	605.91	87%	442.76	235.61
14962	719.5	177.74	85%	457.94	118.72
794	301.18	105.82	81%	460.38	105.58
13646	650.4	113.01	84%	466.4	111.75
15135	628.19	146.12	81%	475.33	93.64
11693	181.61	105.42	82%	480.77	349.7
23390	900.94	286.52	82%	482.87	204.25
6132	287.11	119.69	84%	501.07	132.83
20705	268.91	129.82	81%	501.83	170.59
16518	745.69	208.61	80%	522.4	147.11
24501	924.14	324.29	81%	549.2	118.31
13684	940.24	251.12	84%	561.02	160.11

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TABLE 3D: Necrosis With or Without Fatty Liver				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
23961	413.97	100.86	81%	563.48	84.42
2350	914.43	280.02	83%	566.27	157.14
7262	1171.93	460.29	82%	616.91	222.19
15283	1210.53	436.26	84%	630.12	224.34
4193	484.87	182.86	85%	735.61	136.93
15365	1249.48	437.43	82%	780.82	1098.83
24321	376.06	230.84	83%	789.46	268.88
22559	540.14	342.39	81%	1011.15	343.11
5899	694.24	374.16	80%	1263.41	404.09
7403	704.59	553.96	83%	1286.73	413.15
7199	835.65	469.87	84%	1473.34	421.86
15029	702.04	429.52	87%	1541.16	503.02
4330	675.9	370.63	85%	1565.51	467.91
18002	948.21	459.72	81%	1684.6	511.86
6380	882.65	369.95	86%	1738.14	594.45
16883	1007.86	547.7	85%	1895.14	498.99
6016	963.32	454.45	86%	2023.72	694.11
23261	1077.62	726.72	85%	2102.8	690.37
9016	1096.76	480.03	84%	2344.1	914.36
3062	1684.88	888.35	81%	2819.77	870.18

TABLE 3E: Protein Adduct Formers				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
26190	48.28	140.35	73%	-116.76	71.12
8700	49.85	77.95	72%	-12.19	36.84
1661	36.36	40.61	72%	1.43	29.6
18323	56.4	33.89	74%	6.38	36.18
4348	50.39	34.87	73%	11.17	31.72
17481	36.46	27.96	72%	13.35	33.51
5434	29.26	14.26	76%	13.66	16.78
5930	23.92	9.03	70%	17.21	18.45
15778	24.37	10.62	70%	18.73	13.8
16251	28.52	7.89	78%	20.02	13.7
23315	33.84	16.8	71%	20.08	11.03
23843	65.54	53.1	73%	20.76	16.77
24268	31.94	6.01	72%	20.84	19.94
12185	40.45	26.74	73%	21.92	18.47
6026	60.83	27.25	80%	21.94	33.9
9603	38.75	22.25	71%	21.97	31.16
17747	8.38	6.53	74%	22.43	16.15
21799	-5.84	13.09	81%	23.01	22.31
14195	36.74	19.21	73%	23.09	19.24
3976	17.49	10.74	71%	23.34	30.4
6533	32.77	10.84	73%	23.83	29.19
9166	69.93	53.74	72%	26.99	17.75
4610	63.26	38.33	71%	31.07	36.11
16167	26.11	7.76	73%	34.04	13.5
13967	69.09	21.43	77%	35.02	22.23
17677	-27.82	68.69	74%	36.4	69.93
14449	56.08	25.32	70%	37.77	22.83
11700	55.37	19.55	71%	38.12	21.59
1538	7.74	23.48	75%	38.59	30.39
14053	24.71	9.07	76%	39.07	22.35
6804	17.85	7.18	72%	40.39	128.09
15834	-16.44	51.96	73%	40.56	65.53
23170	43.49	9.26	75%	40.79	23.99
21823	40.81	9.62	70%	41.44	26.15
11485	76.43	21.72	79%	41.78	31.48
26288	55.27	10.43	70%	42.31	15.42
25409	8.36	31.39	76%	43.05	24.65
15251	38.39	9.43	76%	46.23	24.25
8124	57.68	9.64	72%	46.93	19.16
14126	34.95	11.94	71%	47.89	50.38
25203	29.38	13.58	73%	47.94	21.85
9432	100.75	48.6	73%	48.25	28.18
2153	74.75	38.6	74%	49.01	17.57
11127	51.39	6.96	73%	50.24	17.35

TABLE 3E: Protein Adduct Formers				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
2933	50.64	8.95	72%	51.06	22.58
25615	71.69	18.81	70%	52.1	17.72
24654	81.41	24.85	75%	52.19	24.88
15018	84.77	83.88	71%	52.26	40.53
21707	126.24	73.39	70%	59.01	53.51
13918	98.73	44.7	74%	59.06	31.3
10549	42.34	9.93	70%	59.31	64.81
22566	92.71	49.39	70%	60.91	42.33
23304	84.45	28.37	70%	61.03	41.36
25413	37.94	16.74	79%	61.59	20.66
25410	30.99	21.26	78%	62.85	30.41
25411	27.66	23.64	80%	62.98	33.69
13581	83.19	33.57	71%	63.07	26.31
13932	-7.5	82.93	71%	63.9	55.62
14171	74.42	21.1	71%	64.55	37.62
90	36.07	18.79	70%	65.79	40.02
17257	114.03	67.46	70%	67.08	34.52
7537	58.32	14.12	77%	67.47	33.14
25397	33.74	21.21	73%	68.15	31.21
17894	82.35	13.84	78%	68.79	26.36
6814	89.6	32.08	73%	69.88	23.93
21893	44.34	8.05	72%	71.05	72.75
11438	111.77	49.88	74%	71.31	27.16
23324	87.26	41.21	73%	73.64	76.07
4168	104.37	21.68	75%	75.31	30.27
7903	30.15	21.43	74%	75.81	76.12
14335	83.34	14.3	71%	76.03	33.52
24589	112.98	48.88	76%	76.16	48.86
9712	59.65	43.73	73%	76.42	28.63
20980	95.23	16.77	71%	79.04	22.6
6003	97.63	17.55	73%	80.11	26.51
13175	132.4	51.99	72%	81.55	39.28
19315	140.15	42.44	84%	81.73	41.23
15156	110.09	19.69	72%	81.74	31.08
1169	63.7	12.97	72%	82.79	31.48
6032	51.63	16.54	72%	83.57	48.94
17400	145.45	66.75	71%	85.87	52.06
2006	25.42	45.67	71%	86.52	90.27
21068	264.69	160.27	72%	87.31	146.99
11215	-7.35	163.64	72%	87.87	83.21
3074	54.49	18.32	70%	88.91	83.5
22961	111.83	20.67	72%	89.09	31.98
2506	141.66	97.88	71%	91.9	70.92
6409	148.77	36.6	74%	92.24	57.46

TABLE 3E: Protein Adduct Formers				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
22531	91.66	12.53	73%	93.27	36.37
21209	227.02	212.22	71%	95.2	92.15
2383	83.79	16.73	73%	102.14	37.31
11174	184.12	65.2	77%	102.16	98.46
17368	171.8	96.78	71%	103.87	47.72
20851	137.3	28.16	71%	104.02	55.43
3091	153.51	67.82	75%	104.92	90.83
18390	78.71	19.55	74%	106.46	50.88
3073	52.19	23.11	73%	106.62	118.05
6798	135.78	43.18	74%	106.64	46.11
14600	214.24	98.46	78%	109.92	74.91
17617	99.3	12.59	72%	110.02	31.44
14638	87.23	22.1	77%	111.45	74.07
10184	123.58	33.76	72%	112.37	55.43
9170	183.59	55.27	70%	114.2	52.72
22151	79.59	31.13	71%	114.31	59.46
12880	139.94	22.05	75%	114.56	32.47
14937	131.42	66.88	72%	114.75	41.55
2342	166.44	44.77	70%	115.31	58.59
18612	131.39	23.5	75%	116.94	56.6
11691	62.73	41.24	71%	118	79.85
17451	101.96	15.77	72%	120.36	30.67
19566	145.76	30.8	71%	120.45	44.75
24508	154.79	40.91	71%	123.72	32.09
1641	165.12	40.83	70%	128.2	35.55
23885	161.49	29.33	72%	129.48	47.42
20930	134.38	23.9	71%	130.09	61.62
5795	132.03	27.82	71%	130.17	53.46
22051	101.35	28.02	72%	130.68	67.38
26368	145.81	51.6	71%	132.19	91.73
19605	113.2	19.79	72%	133.82	51.82
21040	-18.07	52.54	71%	133.85	229.8
14776	102.58	34.94	70%	134.24	48.08
1223	182.79	51.88	71%	136.08	48.54
13762	158.63	98.43	77%	138.6	59.12
11048	119.54	22.24	73%	142.6	56.03
2292	84.06	42.12	70%	143.71	71.66
17844	277.9	176.64	73%	144.36	79.81
12215	204	107.83	71%	146.76	116.15
2043	179.12	22.45	78%	147.6	36.11
4157	177.19	33.3	74%	147.73	62.63
20711	228.01	78.2	72%	150.83	116.07
26088	145.54	50.27	74%	156.38	187.59
17572	159.65	44.25	71%	158.21	87.38

TABLE 3E: Protein Adduct Formers				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
1690	229.65	95.98	71%	160.28	60.57
15141	173.57	16.39	73%	162.21	36.81
16700	83.29	55.96	71%	162.48	108.7
20380	146.38	29.01	71%	163.02	57.5
15959	167.27	18.31	73%	166.48	70.66
9598	288.09	95.08	73%	168.1	93.9
11590	190.23	28.5	74%	168.24	68.73
22806	131.95	29.2	75%	169.43	77.82
18588	206.23	40.15	73%	170.98	65.63
1141	203.77	31.9	74%	172.68	35.21
9595	271.77	94.28	73%	176.57	69.08
24146	216.8	34.19	71%	177.31	65.74
17291	239.96	109.02	74%	177.33	137.8
21717	206.89	32.09	71%	189.62	69.87
13640	218.18	27.37	72%	190.6	71.83
14007	153.67	25.25	74%	191.38	72.77
16562	238.09	59.35	70%	194.57	50.93
10187	223.84	49.38	72%	198.22	88
25802	244.19	49.71	70%	214.98	65.34
11742	217.52	133.21	72%	216.12	86.16
5020	191.66	26.95	72%	222.98	53.97
22603	221.37	90.45	71%	229.9	65.5
1728	238.87	23.07	75%	230.92	67.51
13534	182.27	33.55	75%	232.74	85.78
2868	286.73	53.61	71%	234.2	69.67
14997	375.7	196	72%	235.84	152.48
5111	393.78	167.65	73%	236.27	143.66
20063	181.07	59.31	70%	236.39	97.14
16780	267.07	94.4	75%	242.2	64.47
23337	207.26	31.63	70%	243.84	91.24
19052	433.77	178.35	77%	253.21	91.88
22619	416.09	190.68	70%	253.69	121.24
6821	297.59	92.7	71%	255.52	167.53
17794	256.5	47.37	72%	259.54	87.89
5110	444.91	212.14	72%	270.46	106.82
4929	215.55	43.79	71%	270.62	101.5
23698	318.89	170.39	75%	278.46	123.55
10594	382.41	57.15	78%	291.69	58.26
6366	466.38	163.71	75%	301.16	141.67
5091	204.8	54.15	76%	305.72	121.65
12317	489.39	140.01	77%	306.86	86.66
15122	284.14	30.38	70%	308.23	65.78
2763	390	85.38	73%	308.26	88.64
20715	439.32	105.47	74%	310.12	180.07

TABLE 3E: Protein Adduct Formers				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
25644	345.9	39.5	71%	314.7	121.98
1175	204.91	111.96	71%	321.32	143.78
24161	356.93	42.23	71%	327.71	79.09
18647	397.22	64.9	73%	330.24	91.79
21281	233.54	99.86	71%	330.78	91.46
4179	625.2	324.6	71%	330.92	127.34
43	237.61	86.82	75%	341.37	75.07
19458	364	43.15	72%	346.08	133.08
23128	313.06	51.91	71%	349.02	136.57
22412	366.89	96.19	71%	351.91	164.5
3143	483.63	141.06	72%	352.34	102.15
6801	355	56.71	70%	360.03	142.03
6066	431.59	75.6	72%	368.47	141.78
21575	432.67	63.41	73%	374.58	82.96
8317	421.43	158.85	72%	379.92	111.94
4371	507.88	124.44	71%	394.01	171.93
11157	373.15	134.06	70%	394.37	101.64
24296	481.18	92.3	72%	403.62	139.39
556	373.54	45.1	71%	408.23	71.6
13055	482.08	75.69	75%	411.9	164.09
8173	519.73	67.84	74%	419.47	110.06
3219	317.14	59.47	73%	426.13	99.03
16278	309.41	102.23	78%	429.92	164.15
23608	566.48	164.2	70%	431.27	241.18
25777	330.46	55.36	76%	441.54	130.73
18522	334.4	99.2	70%	443.31	151.76
6188	512.63	55.77	74%	448.02	139.04
794	333.35	131.81	72%	451.08	111.83
11693	254.85	149.73	72%	463	348.51
14312	397.8	81.06	71%	466.35	160.88
5339	852.55	606.3	72%	468.96	257.55
13646	546.37	100.3	71%	478.7	121.95
22534	444.69	49.89	76%	478.75	159.7
15121	635.12	147.29	73%	513.19	224.34
5038	398.62	86.39	71%	513.52	201.59
7916	483.75	53.88	76%	515.32	200.18
4759	421.47	104.72	71%	536.6	127.07
2339	519.32	64.43	73%	536.85	137.81
16947	444.15	113.82	74%	564.09	119.37
24707	469.06	76.22	77%	596.18	184.62
13557	472.83	125.45	74%	600	181.83
11322	781.82	176.95	71%	605.26	189.58
16623	815.06	113.69	75%	643.07	187.67
20397	756.19	106.73	71%	670.62	123.59

TABLE 3E: Protein Adduct Formers				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
3121	513.81	224.23	72%	698	260.45
6673	697.31	124.67	71%	713.3	302.28
4193	655.24	191.97	71%	718.19	154.45
7552	709.86	131.78	73%	813.29	320.57
820	636.5	127.73	71%	821.94	204.55
19105	924.47	159.69	70%	829.48	236.56
16169	456.68	219.61	72%	862.69	796.4
20503	559	204.67	80%	889.74	380.31
6236	529.47	148.78	79%	903.06	433.66
16879	841.82	418.27	71%	946.87	285.04
17340	1644.38	815.75	74%	997.68	474.22
7451	1340.55	383.41	73%	1014.34	341.2
12306	1456.43	258.06	79%	1024.68	517.58
18905	880.62	169.73	78%	1175.6	278.99
17027	844.61	248.1	71%	1257.61	538.33
22554	997.94	184.01	86%	1359.91	523.26
26147	1510.64	528.64	72%	1410.78	338.29
9192	941.24	221.51	74%	1413.17	565.76
23243	872.48	380.03	72%	1417.04	675.7
16885	1012.98	320.39	72%	1487.91	407.92
15029	1042.74	622.16	70%	1488.18	539.06
4330	1083.48	398.15	72%	1508.27	516.11
22266	1415.56	499.05	71%	1514.02	441.93
18002	1259.73	300.25	77%	1637.82	545.26
4933	1137.93	526.28	71%	1700.05	608.74
21091	1307.31	329.46	70%	1706.98	564.25
6072	1518.7	338.39	72%	1859.25	511.2
17812	1406.92	373.38	70%	1884.53	608.25
17107	1929.94	1307.4	71%	2218.38	823.7
9016	1497.78	482.54	71%	2267.81	949.1
20846	2090.67	1066.14	76%	2478.45	898.34
22558	2580.09	1019.35	72%	2867.4	846.53
6189	1470.69	763.08	73%	2992.11	1673.91
11623	2359.03	1401.37	73%	3039.92	2772.61
16884	1876.68	541.26	76%	3308.78	4455.6
6018	1795.01	783.44	73%	3626.1	3303

TABLE 3F: ANIT Document Number 1650775

GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
22513	633.15	232.37	98%	-132.38	329.17
19388	29.83	17.06	91%	-25.03	31.57
72	49.9	30.74	90%	-17.96	34.45
489	86.15	31.02	99%	-11.18	21.72
11645	46.52	22.15	95%	-10.46	29.11
15003	103.65	34.94	91%	5.13	35.34
4318	23.26	6.71	91%	7.08	9.22
372	43.1	11.62	90%	10.4	12.2
14400	115.49	28.78	96%	12.11	47.49
15480	45.43	16.54	92%	12.38	8.62
22397	98.15	29.08	90%	18.38	61.47
23679	58.03	21.94	92%	20.39	39.25
10790	-79.79	34.37	91%	24	51.35
16006	71.89	13.1	93%	26.66	31.65
15701	115.07	45.82	92%	29.52	22.06
25052	170.78	53.79	98%	31.24	82.74
1221	221.03	65.82	92%	36.47	104.6
23945	98.4	22.42	91%	37.09	29.06
11608	68.37	11.81	92%	39.75	16.9
20741	140.96	42.97	91%	47.33	36.73
5384	110.15	33.33	91%	48.7	63.05
1809	660.39	204.87	91%	51.86	210.98
21088	88.49	15.38	90%	52.62	15.58
488	302.77	84.83	99%	55.29	40.85
20708	69.43	8.17	90%	55.72	21.17
11940	79.89	7.9	90%	56.21	16.71
6585	124.92	40.67	93%	56.76	84.64
15914	167.68	28.59	98%	58.06	29.32
1279	124.99	36.23	92%	60.16	22.09
22487	203.14	70.64	92%	66.54	38.82
17894	123.11	19.61	91%	68.4	25.56
2801	158.72	27.08	95%	68.44	49.17
14465	5.28	16.66	90%	70.62	29.14
15892	279.1	77.25	95%	73.2	79.81
7903	9.08	6.85	90%	75.62	75.73
20772	127.51	24.47	94%	79.34	26.84
11904	152.49	15.73	96%	81.95	37.81
23522	149.93	28.04	91%	84.93	35.96
14017	168.86	47.57	91%	94.1	25.48
23869	219.91	36.9	95%	98.3	110.47
14016	172.79	34.4	91%	101.88	27.02
23005	231.25	60.04	96%	102.75	100.99
24453	296.76	77.39	97%	107.86	52.64
23872	208.24	51.83	93%	110.93	125.84

TABLE 3F: ANIT			Document Number 1650775		
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
10016	224.63	64.84	91%	116.67	48.65
17590	228.93	49.97	90%	127.17	38.31
4944	218.13	56.11	93%	129.57	134.8
15002	208.14	35.44	90%	134.25	36.07
20529	372.92	69.59	93%	138.52	121.65
20849	259.34	55.56	91%	150.94	38.19
15141	216.05	18.73	91%	161.78	36.17
15089	428.71	94.42	90%	164.31	111.52
24779	-119.55	53.79	90%	169.39	275.44
7665	325.89	51.47	94%	171.6	94
12577	530.07	99.18	92%	176.81	126.07
3253	242.21	21.26	92%	177.78	42.54
25069	384.72	63.15	96%	181.27	147.24
23182	70.96	27.02	90%	182.67	82.66
19043	461.37	93.08	91%	184.16	86.52
23445	44.92	13.64	96%	204.01	96.17
22928	18.25	13.42	90%	205.31	168.08
15300	301.52	31.01	95%	208.5	106.84
19073	357.79	55.66	90%	215.38	51.37
24237	602.69	44.81	99%	219.11	138.4
1447	293.32	18.87	94%	221.41	41.58
16408	151.08	35.06	90%	254.15	84.03
23868	529.77	129.48	90%	266.34	657.93
24810	103	36.24	90%	273.16	90.15
5235	460.06	75.16	90%	286.43	79.01
2802	498.79	58.22	95%	287.5	90.87
25747	698.21	163.03	91%	318.26	115.19
2818	510.22	88.82	94%	330.07	92.39
5934	42.22	26	94%	342.34	187.09
1501	711.93	121.22	96%	348.6	117.83
15535	499.6	40.24	91%	391.06	75.12
5437	327.15	25.07	90%	409.5	102.21
12928	607.12	43.69	97%	411.1	97.29
4207	611.82	98.48	90%	440.38	323.23
20701	762.37	110.98	94%	496.87	170.59
1562	360.31	37.96	90%	504.85	111.39
6824	806.51	180.29	90%	506.91	368.25
20983	343.07	66.3	93%	516.16	120.95
13088	199.67	54	96%	593.92	183.67
6613	320.2	65.66	92%	626.43	272.37
25024	451.39	46.56	91%	661.12	185.97
8549	262.14	62.15	93%	665.65	258.33
4193	484.74	47.1	95%	719.76	154.17
2569	257.19	110.15	91%	724.41	288.37

TABLE 3F: ANIT			Document Number 1650775		
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
7892	1166.36	244.14	92%	809.73	244.53
18900	1202.22	137.08	92%	830.76	217.68
16879	540.35	100.54	93%	949.72	286.7
475	635.1	94.59	92%	976.05	230.62
5899	704.5	125.15	92%	1227.29	427.31
3916	883.71	181.1	91%	1427.83	464.67
10378	2563.09	466.04	90%	1469.47	449.7
19363	372.52	212.88	90%	1539.84	830.44
6072	1270.16	177.57	91%	1859.03	508.9
20502	1504.84	383.84	91%	3017.48	1038.48

TABLE 3G: Late Acetaminophen				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
18028	62.86	12.89	98%	11.46	17.68
6151	41.98	5.06	97%	11.63	19.32
1394	46.55	7.94	98%	13.22	8.97
15701	104.85	30.26	98%	29.54	22.64
21586	129.12	22.29	98%	37.42	35.11
18099	74.54	10.03	98%	37.77	12.82
18990	191.58	50.21	98%	37.78	56
5492	154.99	36.3	98%	42.55	45.33
16958	152.1	24.97	99%	48.17	21.95
25892	5.84	14.89	97%	52.01	13.92
4281	8.04	4.69	97%	52.71	20.31
20817	552.74	204.49	99%	56.23	83.19
494	-58.87	15.28	99%	57.66	57
17091	221.12	37.22	99%	64.55	35.7
5493	201.07	32.69	98%	68.52	42.64
4650	257.12	41.99	98%	74.24	55.94
20818	387.65	157.18	99%	81.37	42.47
8356	191.89	39.3	98%	81.94	31.64
17090	166.91	23.91	98%	82.55	25.23
6153	47.01	7.23	98%	89.68	30.74
1399	422.27	102.52	97%	118.53	72.23
18369	14.78	33.12	98%	154.92	43.99
8107	82.52	12.58	99%	157.67	30.22
21305	78.03	11.47	97%	162.22	42.69
16219	91.23	10.22	97%	162.24	35.05
20380	51.46	16.74	97%	164.24	55.84
14970	64.35	7.2	98%	165.35	37.88
11039	22.92	14.76	98%	165.75	75.12
1644	69.04	14.22	99%	166.93	43.07
25632	23.75	9.64	100%	170.77	437.48
25069	648.62	107.28	98%	177.18	137.77
12848	77.84	12.22	98%	178.82	51.97
15571	37.5	7.71	100%	182.36	613.17
5998	82.64	16	98%	198.22	47.74
1542	75.63	15.75	97%	201.9	67.93
11429	113.75	15.07	97%	220.8	45.17
11635	84.37	10.31	100%	235.11	58.7
24246	680.67	154.62	97%	235.68	110.38
17684	115.68	11.83	97%	243.52	58.44
1479	111.19	13.1	98%	246.79	62.43
16023	118.74	16.82	97%	262.5	67.56
20986	100.65	16.03	98%	269.03	97.64
23033	164.75	20.5	97%	269.22	53.32
24810	78	27.42	97%	273.76	89.28

TABLE 3G: Late Acetaminophen				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
8592	97.92	12.74	99%	275.69	78.69
12156	66.84	25.24	99%	279.94	158.15
20555	74.21	32.18	97%	280.75	96.14
18837	70.96	24.35	98%	281.18	112.85
17758	47.9	17.49	98%	283.74	151.83
11152	89.81	23.98	98%	284.55	88.62
22582	97.84	15.79	98%	290.41	88.62
6155	86.76	17.03	100%	302.82	149.97
10093	894.21	296.81	97%	307.41	125.35
23854	518.98	43.24	97%	317.71	83.8
4314	161.66	22.27	99%	325.66	70.88
20864	896.29	162.64	98%	340.85	169.02
9072	134.11	29.83	97%	372.6	132.4
15462	187.89	20.53	99%	377.51	69.64
3023	74.88	27.06	99%	377.75	123.14
1529	196.76	20.46	97%	378.11	72.49
24670	211.91	19.4	98%	380.22	75.72
25480	139.68	36.79	97%	384.92	88.4
4224	217.33	27.1	98%	385.39	68.02
1653	161.77	30.91	99%	413.84	133.06
9905	215.17	33.74	97%	417.78	81.53
11153	184.99	26.78	98%	424.64	112.76
21977	167.03	43.78	97%	425.7	100.74
21950	225.05	28.55	97%	431.25	83.14
2505	181.37	17.8	99%	437.97	99.3
794	185.22	23.41	98%	452.2	109.84
5920	1687.13	555.96	99%	456.93	241.47
2667	266.65	38.11	98%	472.54	95.54
24722	177.21	38.39	99%	491.55	112.03
23390	1178.14	133.27	98%	504.75	225.74
1562	261.12	32.84	98%	506.49	108.81
15113	155.11	52.14	98%	515.14	163.96
4199	289.55	26.97	98%	519.47	108.02
8872	1732.12	253.22	99%	539.58	281.13
24771	204.77	35.86	99%	548.56	123.7
13088	127.47	50.84	97%	595.53	180.73
17541	1185.11	145.34	98%	686.63	152.47
24811	244.05	55.21	98%	713.37	236.19
24321	133.15	53.97	98%	767.37	279.51
7552	180.78	39.85	98%	820.01	310.92
19732	145.53	28.91	98%	918.79	410.43
11205	330.78	77.32	97%	976.22	280.85
15673	1721.01	183.17	98%	1022.66	229.71
14512	230.44	36.6	99%	1088.1	390.72

TABLE 3G: Late Acetaminophen				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
11850	2429.93	244.48	98%	1189.68	370.45
633	647.11	128.95	97%	1346.47	304.28
14960	3443.82	469.79	99%	1352.48	446.55
22554	383.07	75.73	98%	1365.63	511.2
24049	4317.73	1756.71	97%	1441.54	440.22
2587	661.56	121.75	98%	1598.85	493.87
12314	743.43	156.24	98%	2014.22	647.46
15315	4723.83	784.41	97%	2482.27	635.01
17730	6017.72	1076.55	98%	2933.25	821.08
6189	422.42	136.09	97%	2994.06	1657.8
20873	5487.66	1292.77	97%	3014.46	6409.47

TABLE 3H: Early Acetaminophen				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
21175	8.2	4.71	94%	28.82	12.57
7528	8.32	4.93	95%	34.66	16.43
20282	-15.7	9.27	92%	36.02	33.93
5966	-2.42	11.53	95%	36.31	21.84
22695	10.13	6.89	92%	38.79	17.51
15634	1.39	5.65	94%	39.68	19.47
1520	15.99	5.3	94%	47.93	19.37
16524	20.02	6.63	94%	48.44	13.24
18482	16.24	5.44	95%	48.47	17.05
2280	19.83	5.96	93%	49.02	23.16
19787	15.18	6.28	94%	50.55	15.04
18584	6.53	10.13	95%	51.53	23.14
13926	21.46	6.96	92%	52.65	14.76
11423	15.02	8.15	94%	56.28	19.95
11940	21.79	9.2	93%	57.53	15.9
23000	22.53	12.08	93%	57.77	15.01
3080	-6.92	14.95	93%	58.31	48.7
23710	158.41	53.72	92%	58.38	71.02
23047	15.29	11.17	95%	58.49	16.56
16566	17.77	6.03	98%	58.51	15.69
19650	-70.3	47.02	93%	61.72	44.09
15467	11.36	7.01	95%	62.46	46.17
16728	14.72	12.75	92%	64.03	32.75
13568	28.12	10.02	94%	67.08	17.03
13932	-112.44	63.3	94%	67.38	48.47
15139	21.25	9.99	96%	68.11	25.84
24079	25.3	8.6	95%	69.08	26.17
22487	6.73	8.7	98%	70.08	41.42
14139	19.82	7.55	95%	71.65	22.54
15181	26.59	10.69	94%	79.78	30.61
23077	38.94	17.17	92%	81.22	21.14
17158	17.52	10.77	94%	83.01	45.36
20971	43.32	10.04	92%	83.29	21.37
1169	27.52	12.64	92%	83.96	30.23
16871	19.55	12.49	93%	85.46	26.85
9164	27.2	10.23	95%	85.81	27.4
15980	26.43	18.24	93%	86.7	23.87
16361	43.56	12.22	92%	91.15	25.64
21321	27.09	14.56	93%	105.32	56.02
3486	34.72	10.49	97%	107.9	41.25
2727	45.87	10.75	92%	110.53	48.76
8597	69.34	16.36	93%	116.43	40.21
574	65.57	6.51	93%	117.45	179.89
8730	45.4	17.81	92%	119.22	42.05

TABLE 3H: Early Acetaminophen				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
13351	36.93	12.29	95%	122.54	50.81
6330	28.64	17.18	98%	123.06	58.01
18829	33.89	17.14	94%	128.07	58.85
16134	18.36	24.36	94%	128.31	40.65
20975	70.64	13.75	93%	135.77	31.44
64	64.42	13.23	93%	141.31	35.51
11426	36.73	16.99	94%	143.85	61.64
4127	42.82	25.2	92%	147.26	55.78
2043	94.32	14.17	93%	149.89	35.38
25814	49.58	15.47	93%	150.18	60.26
23044	256.5	54.33	94%	154.34	33.61
23491	80.29	14.78	92%	156.45	57.06
21909	77.01	15.95	92%	157.72	48.89
16364	54.12	18.74	92%	161.04	68.62
6861	53.34	24.76	95%	173.75	47.49
23709	365.56	102.97	92%	174.65	139.26
18981	80.53	12.18	98%	180	124.54
18136	92.28	22.73	96%	180.63	44.47
15170	63.67	31	93%	182.69	57.04
15491	50.3	18.75	94%	184.71	62.38
13640	81.51	25.5	94%	194.43	69.6
1542	110.94	15.7	93%	202.72	68.33
23711	965.1	437.75	93%	203.15	366.12
3549	100.08	20.01	93%	203.26	64.36
5749	105.17	17.76	96%	203.46	50.97
1921	469.15	75.54	94%	203.88	88.71
5953	1395.67	589.94	92%	204.16	203.2
11179	51.98	16.53	97%	213.56	68.01
17571	121.22	22.36	91%	215.28	47.28
1919	540.5	142.58	94%	224.99	91
16449	-17.52	49.15	92%	225.71	118.83
7927	58.81	47.71	94%	235.03	77.05
8735	104.51	40.55	92%	260.2	118.96
15070	64.72	20.64	92%	276.22	127.77
23606	645.68	142.54	92%	308.45	97.73
4291	55.74	33.3	95%	309.48	143.72
6366	132.6	38.47	93%	309.95	143.06
22862	102.99	68.89	92%	331.29	84.1
1920	699.35	125.66	94%	334.22	116.2
23230	101.11	53.57	94%	347.39	161.95
1802	68.01	68.24	93%	348.21	129.82
1501	135.65	55.72	93%	359.59	120.35
3143	180.22	37.55	93%	360.43	101.81
20799	195.78	28.73	95%	368.39	68.29

TABLE 3H: Early Acetaminophen				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
21980	205.1	26.69	96%	380.01	105.72
4234	728.11	88.4	91%	441.47	146.01
16215	277.82	31.3	92%	468.47	103.74
25705	303.85	36.79	95%	471.16	88.31
164	290.9	32.23	97%	476.12	84.6
21097	844.93	124.78	93%	521.05	142.52
23139	297.32	105.82	94%	614.3	226.46
8549	197.64	79.57	92%	674.01	251.68
9190	372.68	47.07	94%	1016.16	415.34
6291	552.9	84.63	97%	1091	307.85

TABLE 3f: Late Carbon Tetrachloride				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
17064	50.24	16.97	96%	-4.18	20
1625	114.41	34.24	99%	0.07	12.89
5885	38.36	18.29	97%	1.99	9.82
18046	46.73	12.92	99%	2.71	14.04
16649	220.02	92.9	99%	3.43	37.53
1554	47.01	20.46	98%	4.33	6.64
20950	54.4	13.02	98%	6.19	12
13458	58.51	18.25	97%	6.84	20.17
6879	53.86	20.46	98%	10.45	8.61
2065	77.67	43.56	98%	14.07	10.39
16654	153.26	64.25	99%	14.11	9.91
23651	330.28	228.17	97%	21.42	37.58
15312	116.71	36.41	96%	25.99	29.2
21818	119.6	30.36	97%	26.66	21.99
4048	1573.97	2042.27	100%	28.72	92.76
21695	174.77	50.28	99%	30.87	22.35
1126	93.96	18.28	98%	31.78	16.86
17157	116.08	34.36	98%	33.37	18.38
21586	155.13	41.01	98%	35.85	31.46
4097	202.62	143.18	96%	36.77	20.82
20589	204.58	80.85	99%	39.66	14.51
4856	195.72	58.45	98%	44.87	22.87
17500	1.65	7.49	96%	45.77	44.45
16730	154.98	38.01	97%	46.39	26.25
20449	440.43	164.04	98%	47.45	46.4
15655	237.45	149.71	98%	48.19	26.25
19040	396.02	114.12	99%	54.95	29.77
1037	191.13	61.49	99%	55.16	22.83
4178	263.2	73.51	99%	58.46	46.4
23302	134	32.72	97%	60.71	24.04
21060	195.49	44.63	99%	66.73	22.3
2781	300.75	90.51	100%	67.08	21.7
1571	306.34	84.06	98%	69.24	44.27
1258	201.18	53.89	99%	69.76	26.45
20755	315.54	99.4	98%	70.92	37.08
21416	180.67	33.54	98%	71.26	32.81
4327	209.63	44.69	97%	73.46	30.98
2853	243.76	74.49	99%	79.5	27.62
14458	462.45	169.29	97%	79.77	81.9
17956	135.44	24.53	96%	80.41	19.61
16650	335.98	95.22	99%	82.71	42.71
8152	184.75	44.1	98%	84.34	21.12
22321	565.88	166.7	98%	90.43	44.8
20801	244.26	53.66	97%	93.54	45.27

TABLE 31: Late Carbon Tetrachloride				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
15203	217.53	41.56	99%	94.08	22.2
16683	214.61	51.64	98%	96.97	26.38
7690	485.59	136.48	97%	98.07	100.2
18705	230.49	55.83	99%	103.84	19.16
574	566.67	151.26	99%	104.84	163.13
20644	284.09	69.38	96%	104.86	53.3
12613	385.02	81.17	98%	105.74	49.08
23173	527.13	156.81	99%	112.95	62.38
10016	305.83	117.64	98%	113.41	37.12
25257	401.37	69.21	98%	123.93	52.05
19377	245.39	39.45	98%	124.66	31.89
25313	368.62	55.36	99%	125.11	47.2
23888	323.47	71.72	99%	127.05	34.78
17754	280.21	65.27	98%	127.56	39.49
20891	284.25	57.73	96%	128.54	57.37
19241	305.11	61.55	99%	128.91	25.25
17369	251.93	28.1	96%	130.99	61.88
4049	1800.21	615.67	99%	131.28	173.33
4426	226.63	33.81	98%	134.21	26.79
15282	495.77	127.65	97%	140.76	88.42
20849	288.07	45.99	98%	148.97	33.86
17225	314.55	56.91	96%	156.73	51.3
24388	756.8	218.92	98%	158.69	122.1
16854	274.55	32.55	98%	161.83	29.13
16610	376.93	79.48	97%	165.18	49.27
6193	447.67	59.78	99%	194.57	54.15
3549	368.01	54.43	97%	196.19	60.45
2744	487.89	65.94	98%	202.98	55.42
15281	509.13	65.19	98%	207.9	69.15
17571	337.5	57.58	97%	209.52	44.91
8928	323.46	31.08	98%	210.05	36.77
25802	411.96	57.18	98%	210.79	57.41
12551	48.43	13.62	98%	212.69	71.68
7602	453.04	80.74	97%	213.06	62.29
15543	555.28	110.77	97%	219.06	83.33
958	492.73	90.77	98%	234.42	59.68
2854	520.08	129.87	99%	239.21	54.99
5331	517.46	66.57	99%	253.08	62.49
23013	631.62	255.14	98%	253.69	77.98
19768	497.6	88.61	97%	258.31	86.39
18107	475.79	86.06	98%	270.37	50.73
10306	537.72	79	97%	270.7	72.51
3138	773.53	129.57	99%	280.59	128.8
16684	591.01	105.06	98%	303.32	77.67

TABLE 31: Late Carbon Tetrachloride				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non-Group Mean	Non-Group Stdev
23854	563.93	104.51	97%	314.55	77.09
20897	602.65	120.81	96%	315.7	85.83
19298	835.39	188.74	97%	328.8	152.97
25718	579.2	77.87	98%	328.95	68.42
14959	676.74	116.99	97%	377.46	94.35
20879	73.93	55.35	98%	390.34	126.05
6824	1794.5	585.37	97%	479.02	298.25
13684	1052.78	207.71	96%	578.09	181.33
16438	1299.24	155.02	99%	582.93	144.92
4193	332.28	95.67	96%	726.26	144.3
7552	163.75	89.31	97%	826.93	304.52
16883	681.46	275.09	96%	1856.78	528.87

TABLE 3J: Early Carbon Tetrachloride				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
8663	721.93	225.97	97%	-87.65	146.96
8662	653.64	143.71	99%	-66.58	95.42
1727	348.89	185.42	95%	-57.26	75.16
11493	129.55	67.26	96%	-32.97	39.87
2628	251.75	147.92	96%	8.65	34
15647	109.5	26.81	94%	11.25	155.64
13265	78.29	37.64	97%	12.05	9.28
923	199.22	94.23	95%	15.81	23.49
8661	614.42	215.98	99%	16.84	60.47
7301	187.05	149.7	95%	19.02	15.94
15312	129.52	34.52	94%	23.98	24.69
1305	159.8	80	94%	27.12	24.91
1598	232.56	58.02	96%	28.01	58.64
23567	918.41	595.26	94%	30.79	97.73
25198	145.62	46.46	97%	31.18	21.37
22443	413.57	187.24	96%	32.31	38.97
809	170.72	83.79	94%	33	26.32
18043	157.01	66.2	95%	35.05	27.16
16825	86.21	14.87	95%	36.95	15.49
11494	365.78	87.61	98%	39.57	52.58
12969	315.69	145.09	97%	39.62	30.17
347	94.32	20.45	94%	44.31	19.5
15313	188.23	47.79	95%	44.81	34.49
25907	196.63	51.46	96%	45.95	29.69
2629	258.22	130.51	94%	47.27	31.18
4119	172.99	53.46	96%	49.1	27.57
15617	131.28	26.96	94%	49.13	28.01
11483	356.15	129.53	95%	49.85	57.22
25098	263.21	101.83	95%	51.71	35.09
8664	685.72	187.22	98%	51.77	117.57
7806	173.92	56.36	95%	51.78	24.26
5932	142.26	26.26	94%	51.91	24.37
18501	128.83	31.95	94%	53.7	17.47
352	306.66	117.09	94%	53.93	48.46
3831	120.45	24.02	95%	55.42	25.76
651	234.03	95.8	96%	55.88	31.26
650	252.68	84.65	96%	57.08	37.09
17337	140.87	38.01	95%	60.97	56.3
7036	176.78	42.65	98%	62.22	22.87
22124	125.04	23.89	94%	64.53	17.38
23587	208.43	60.7	94%	66.37	32.19
21130	369.23	131.33	98%	72.63	40.41
353	475.4	152.81	94%	76.96	69.6
1183	426.68	140.86	99%	78.14	33.96

TABLE 3J: Early Carbon Tetrachloride				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
16080	464.2	128.58	94%	81.55	87.93
18349	210.66	61.07	98%	82.84	26.6
19184	623.72	284.24	97%	83.93	71.71
2788	214.08	67.37	95%	87.98	29.5
15291	225.71	67.73	96%	89.73	24.64
21380	195.27	36.2	95%	90.84	24.55
17908	489.98	67.94	99%	91.5	64.42
1475	764.62	270.51	94%	95.88	162.38
354	549.22	181.76	94%	96.35	76.24
14424	1887.85	604.98	95%	104.46	294.14
23438	233.78	45.73	94%	105.37	42.63
19085	235.47	46.91	96%	105.97	34.08
16318	569.79	137.14	98%	106.93	68.65
19641	354.6	119.72	94%	111.15	52.02
2049	351.74	96.17	96%	113.35	54.16
22625	588.59	137.7	98%	119.99	73.04
15616	363.79	100.12	94%	126.33	57.91
16081	590.52	148.03	94%	131.04	114.9
1306	354.57	112.94	96%	131.39	47.78
5489	361.63	79.95	96%	135.76	55.44
19086	312.97	47.23	96%	137.05	43.97
22681	1733.5	1045.76	94%	138.8	233.99
25567	440.46	120.5	94%	146.39	68.31
5820	392.73	112.42	94%	148.03	58.75
19075	541.95	182.12	95%	149.36	55.34
8314	4119.47	2769.99	98%	151.41	501.27
24234	520.49	130.96	97%	152.5	60.67
15490	337.2	71.58	94%	153.12	62.58
18259	558.61	152.63	96%	160.23	83.57
4952	867.67	202.68	94%	163.05	167.45
20795	498.26	84.68	97%	165.95	99.22
15292	331.21	64.99	94%	168.13	43.41
17735	616.97	206.23	95%	170.62	159.27
15382	2086.55	655.12	96%	179.06	342.56
6892	472.18	95.02	96%	185.03	58.03
10019	573.47	205.58	98%	186.54	69.46
8984	284.45	40.11	94%	186.61	41.02
3587	1589.64	832.55	95%	189.25	164.29
23331	343.71	75.44	96%	197.53	41.31
17753	422.58	107.22	94%	199.72	55.6
3430	482.45	99.02	96%	205.47	61.75
5937	398.98	79.16	95%	210.95	55.18
15091	457.85	75.14	94%	214.95	79.48
2615	475.24	65.04	95%	217.68	61.55

TABLE 3J: Early Carbon Tetrachloride				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
22177	437.19	83.23	94%	220.99	76.02
15558	421.96	49.45	96%	261.21	89.18
15171	2476.94	637.89	99%	267.37	221.89
24235	651.38	135.2	94%	281.24	89.88
15172	1130.82	386.63	99%	294.17	160.06
8665	2451.27	808.98	94%	320.3	582.92
3816	941.08	189.07	97%	375.12	97.06
15051	1917.64	600.05	97%	421.84	274.9
6321	1227.19	294.21	96%	436.54	171.1
11495	1157.08	222.69	95%	479.89	170.9
19012	1131.9	195.46	95%	491.44	164.34
3139	3078.65	1586.03	96%	683.5	401.95

TABLE 3K: Late Cyproterone Acetate				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
25183	57.99	11.18	99%	-65.21	41.14
9969	66.32	43.47	97%	-28.99	30.94
19292	39.25	15.99	99%	-0.31	8.76
1749	36.95	4.96	97%	6.56	12.85
9697	56.57	15.67	98%	10.84	13.14
19465	72.95	28.72	97%	20.05	13.1
15441	57.11	16.22	98%	20.18	10.67
15987	363.79	45.36	100%	34.51	32.07
13580	0.18	7.99	96%	36.01	21.03
16319	89.11	16.96	97%	40.72	16.75
3510	7.29	10.94	97%	41.17	13.42
906	86.53	14.25	98%	49.56	12.1
19053	13.57	5.47	95%	50.36	50.88
5824	209.96	52.5	99%	54.58	27.78
17685	17.67	8.55	98%	59.93	29.82
4588	22.45	6.38	97%	60.62	24.09
14250	25.11	4.35	96%	61.29	33.6
17091	228.81	44.44	99%	65.14	36.75
4312	458.51	102.72	98%	74.88	65.39
6667	35.58	7.42	95%	79.42	27.4
9668	25.68	7.88	95%	82.74	43.74
17090	174.43	31.41	98%	82.84	25.5
14840	25.84	4.54	97%	84.25	56.66
18906	165.1	25.73	97%	86.57	33.68
21184	24.35	7.77	96%	88.84	44.65
11960	-21.76	29.8	98%	91.47	36.61
17092	282.98	55.61	99%	100.94	37.11
18316	41.41	4.56	96%	101.42	51.02
11724	26.29	6.1	97%	107.83	53.24
21238	29.51	14.62	96%	107.94	65.27
9015	50.88	4.22	97%	111.21	39.72
22204	31.75	11.16	96%	111.85	67.38
21228	60.32	10.12	95%	127.7	59.24
25725	303.56	97.38	99%	127.99	39.22
3381	215.51	15.65	98%	129.07	31.01
14199	49.89	11.18	96%	129.55	63.16
12158	539.59	79.37	98%	149.3	94.76
20711	15.4	13.95	97%	153.96	115.63
25055	543.96	83.34	98%	160.37	97.11
15955	401.03	64.61	97%	167.69	104.75
10002	79.22	8.3	96%	169.5	85.35
15888	103.8	7.37	96%	174.62	107.57
23709	91.99	7.53	96%	180.95	142.33
19255	96.69	11.59	96%	191.17	81.51

TABLE 3K: Late Cypoterone Acetate				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
16124	59.91	18.31	97%	198.11	129.25
8053	55.5	21.16	95%	199.73	121.49
1796	713.84	124.8	99%	202.3	82.74
6431	44.99	10.12	99%	211.22	232.8
4576	60.8	23.4	95%	213.43	78.15
22713	83.58	18.05	96%	218.87	74.81
20803	489.88	37.25	100%	230.7	84.72
8905	129.45	13.33	96%	236.42	105.34
16780	482.97	115.87	98%	240.36	60.06
1479	143.4	14.02	96%	245.89	63.54
12156	947.53	169.32	98%	270.19	144.04
24860	762.67	137.57	99%	271.87	106.81
20744	131.35	9.57	96%	277.11	153.4
12157	890.46	241.3	96%	295.84	176.52
19256	169.36	16.84	97%	300.56	93.48
12155	849.1	121.68	98%	328.83	112.43
1795	886.32	169.03	98%	332.97	138.76
20864	838.11	192.14	98%	343.82	174.37
23032	174.66	35.02	96%	348.75	98.36
18860	658.47	93.14	97%	352.87	102.72
6801	167.82	26.32	95%	361.85	140
20915	707.08	113.27	95%	376.44	136.93
20707	836.46	117.26	98%	382.05	142.91
18473	830.53	86.28	99%	405.69	223.02
16278	872.29	116.7	98%	422.72	158.18
20041	189.58	32.85	98%	435.36	136.08
25056	1055.84	195.39	98%	435.67	129.34
20714	148.21	41.46	96%	438.15	637.41
15500	239.22	24.81	97%	456.63	119.52
15755	214.37	34.27	99%	457.32	99.49
11693	37.65	37.02	96%	462.5	345.74
15127	911.94	86.23	98%	466.74	134.84
21078	321.33	18.18	96%	470.87	98.57
19012	218.63	26.43	98%	519.87	206.37
20713	192.33	64.34	97%	523.9	200.74
8872	2206.69	222.08	99%	539.95	267.56
1551	300.22	24.52	98%	540.56	133.08
15391	748.88	48.29	98%	555.42	79.76
17541	1121.82	231.52	96%	689.41	156.88
2569	1283.55	169.03	96%	712.78	286.97
20804	2441.26	676.23	98%	723.52	393.32
12160	2592.66	403.1	99%	826.97	370.84
11644	421.94	97.8	96%	834	240.59
17788	2318.81	523.51	98%	909.78	263.72

TABLE 3K: Late Cyproterone Acetate				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
17117	1568.35	191.58	96%	1006.34	230.44
15645	474.3	53.72	99%	1085.08	601.13
6479	446.51	75.83	98%	1215.32	472.08
22266	2441.41	319.93	97%	1502.46	434.41
21798	2671.47	378.77	98%	1532.27	351.77
1957	451.84	140.88	95%	1533.47	786.6

TABLE 3L Early Cyproterone Acetate				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
12375	39.55	6.91	93%	6.16	21.17
2803	101.95	30.32	98%	12.74	30.67
18685	55.02	18.44	95%	16.95	33.49
15162	38.84	5.14	93%	19.37	14.99
10200	71.52	14.25	98%	21.52	18.12
11619	40.76	5.29	93%	24.39	9.81
5018	43.56	9.08	93%	25.12	11.36
11125	95.81	17.05	97%	28.28	20.68
25706	108.93	17.96	98%	28.74	24.94
17506	202.1	34.4	99%	28.98	70.24
25852	57.42	8.81	96%	29.52	10.16
16783	107.34	24.04	95%	33.35	33.97
4725	93.9	10.69	96%	40.84	123.37
15097	97.88	13.08	95%	42.76	28.79
2594	115.78	19.67	97%	43.16	28.35
18484	139.66	35.48	98%	43.46	17.72
7967	80.61	8.41	93%	45.01	25.09
15251	113.13	7.4	98%	45.58	23.44
14913	104.39	13.3	94%	51.71	28.53
15655	103.19	9.18	98%	52.4	44.96
5740	98.42	10.02	93%	54.17	22.49
15433	88.27	7.53	96%	55.12	26.88
6676	81.6	7.48	94%	55.36	26.6
12203	284.85	67.35	98%	57.37	50.59
11876	164.99	37.72	97%	59.91	38.15
24051	156.13	27.52	97%	60.29	28.94
24227	159.76	22.26	98%	64.47	29.99
23160	140.18	19.33	94%	79.22	46.25
24236	118.22	13	94%	79.8	46.11
5754	354.87	77.25	99%	82.05	52.7
5046	201.39	29.93	96%	91.8	52.22
4679	155.83	15.02	94%	93.09	39.05
2372	227.9	45.92	97%	99.62	37.53
466	147.74	16.09	93%	100.97	24.77
9128	497.34	121.83	99%	101.85	43.69
16087	72.43	6.68	96%	105.7	17.95
22898	203.84	9.33	98%	107.87	73.23
22717	160.84	13.59	94%	114.08	91.92
9775	472.31	82.29	98%	118.73	84.58
19605	335.27	35.78	99%	131.91	48.58
22503	297.45	72.36	96%	134.1	70.26
1903	323.28	80.7	97%	134.88	55.57
6582	298.97	43.04	96%	137.13	83.58
15030	175.94	7.66	94%	138.35	50.24

TABLE 3L: Early Cyproterone Acetate				Document Number 1650775	
GLGC ID	Group Mean	Group Stddev	LDA Score	Non Group Mean	Non Group Stddev
18235	287.07	66.63	97%	138.94	38.25
15282	203.3	21.11	94%	148.94	105
13799	391.75	74.97	99%	152.36	52.97
17955	257.17	57.57	93%	154.46	62.37
6272	415.31	82.23	98%	157.51	61.87
3266	238.25	22.7	93%	160.5	50.15
15959	389.2	63.99	97%	164.9	67.38
1884	191.9	7.86	93%	166.42	45.16
15955	294.4	26.85	95%	169.12	106.78
9486	468.68	91.29	94%	177.99	126.67
21275	349.64	80.81	96%	178.44	97.42
16053	311.13	32.05	96%	206.21	223.6
16747	445.78	87.8	96%	210.09	78.61
20350	393.34	72.05	94%	217.18	69.07
6855	290.54	8.31	95%	227.55	64.59
2326	437.32	39.57	98%	229.27	188.62
20063	579.31	78.7	98%	232.67	92.42
11403	386.09	85.89	93%	235.8	240.72
14303	381.51	38.02	94%	240.55	89.2
5696	167.33	17.35	93%	246.96	110.75
7586	568.83	104.54	95%	247.96	137.64
6821	667.02	106.37	96%	253.55	163
12956	525.48	76.44	96%	256.59	86.57
11404	487.51	32.83	97%	257.84	173.77
4092	428.51	31.72	96%	269.02	120.09
20	182.6	13.17	93%	280.26	77.1
7003	480.07	48.06	93%	299.91	136.85
22835	515.95	104.87	95%	316.8	87.86
22235	511.17	15.69	98%	321.64	119.46
1900	909.26	49.41	99%	339.05	159.22
9674	997.96	198.11	93%	345.29	332.5
2757	553.61	62.46	93%	349.8	112.21
3233	469.14	29.71	94%	350.16	111.19
4937	644.14	96.95	97%	351.09	99.81
16688	485.77	14.98	95%	367.52	115.86
8215	528.57	63.29	95%	395.11	169.02
23515	527.7	47.35	94%	399.57	182.28
22548	1110.25	157.18	97%	429.36	198.23
25056	701.5	107.45	94%	439.98	142.37
23030	298.12	25.05	94%	443.27	320.1
1930	795.75	79.48	96%	488.29	180.53
22379	987.52	105.4	98%	497.46	281.53
18280	625.22	42.6	95%	500.51	355.18
13557	431.55	35.49	94%	598.3	181.76

TABLE 3L: Early Cyproterone Acetate				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
1901	1382.54	291.7	97%	621.54	268.35
16205	433.92	33.39	96%	622.45	128.79
19069	172.52	18.28	97%	622.95	345.06
22906	1189.14	110.88	96%	633	508.28
7262	974.62	93.19	94%	656.38	287.35
2354	1225.56	104.8	96%	666.98	252.59
7362	563.59	37.8	94%	816.77	299.68
15345	1802.55	235.04	95%	907.53	318.35
3803	1252.52	61.21	95%	914.67	209.78
22929	620.51	53.83	95%	1008.19	813.54

TABLE 3M: Late Diclofenac				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
22513	2558.9	1121.55	99%	-137.91	262.53
19512	46.17	16.3	99%	-20.41	27.06
8700	150.91	57.74	98%	-11.7	37.23
19715	70.75	11.06	98%	-11.14	18.14
11645	79.3	16.37	99%	-10.24	29
20200	64.31	15.52	98%	-7.94	37.09
7858	64.65	32.07	99%	-1.01	21.41
22516	230.66	81.61	99%	0.06	50.52
18974	52.85	14.89	98%	1.86	14
5291	56.16	15.92	98%	7.46	12.49
9977	33.87	1.2	99%	9.6	16.15
372	53.19	3.15	99%	10.58	12.35
14400	168.71	36.04	98%	12.55	47.33
955	44.09	5.41	98%	13.21	12.09
26320	148.57	67.07	98%	20.83	30.04
23555	177.11	52.37	99%	22.61	21.13
10790	-147.58	11.69	99%	23.65	51
21445	152.54	38.45	99%	24.94	41.96
16173	102.32	21.29	99%	25.18	32.39
25052	653.33	363.97	98%	29.48	65.56
3452	158.59	24.76	99%	29.79	27.82
12277	126.55	32.95	98%	30.14	31.31
16240	-1.46	1.38	98%	31.65	28.31
22512	280.38	149.23	99%	44.34	59.45
7056	-11.07	4.54	99%	47.11	28.14
19411	117.91	13.87	98%	47.27	27.38
6198	184.84	21.67	99%	47.55	71.13
25246	17.4	2.21	98%	50.19	18.57
15504	223.77	86.68	98%	54.96	108.78
22514	404.55	221.07	99%	61.23	63.25
13045	-1.13	17.95	98%	64.8	29.82
9826	-2.67	5.61	99%	66.89	26.12
8079	-12.12	4.26	99%	70.37	43.83
2310	520.93	356.23	98%	71.67	85.7
25290	159.42	12.09	98%	74.09	78.6
1430	-67.02	9.22	98%	76.13	70.5
13895	199.32	16.84	98%	81.85	53.19
11904	162.22	8.31	98%	82.4	38.06
11596	208.15	21.91	98%	92.32	36.27
22515	1549.73	711.86	98%	100.85	133.92
22321	175.23	33.28	98%	101.48	89.03
8522	399.56	124.51	99%	108.85	69.48
14491	261.16	27.37	98%	115.78	52.28
21228	330.87	20.94	99%	125.87	57.45

TABLE 3M: Late Diclofenac				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
20529	887	406.86	98%	137.26	107.43
3250	366.5	30.94	99%	144.45	58.3
14504	691.37	422.61	99%	151.43	95.9
26133	549.15	106.67	98%	153.02	280.02
21978	81	5.94	98%	160.08	42.54
3708	397.54	42.39	98%	161.72	77.01
396	355.91	58.85	98%	172.48	57.78
23889	72.55	12	99%	175.14	49.66
12577	1097.35	411.24	98%	176.09	109.22
18580	822.77	189.24	98%	201.23	172.81
24237	928.14	321.39	98%	219.99	132.72
25618	180.02	2.6	98%	245.62	81.24
4969	1833.13	949.96	98%	265.19	240.61
5110	738.94	147.68	98%	271.77	107.36
25619	193.88	2.98	98%	274.38	108.29
13353	101.42	6.77	99%	275.78	68.9
7225	610.95	103.39	98%	276.52	112.14
1175	89.72	12.52	98%	319.98	143.49
4314	199.22	16.19	98%	324.04	72.64
21281	119	14.89	99%	329.77	91.62
699	744.08	166.35	98%	385.87	84.98
17281	191.29	11.48	99%	407.86	108.78
7697	126.05	9.16	99%	418.46	147.54
24012	650.52	28.61	99%	423.59	476.52
5339	1561.45	746.53	98%	471.48	259.27
1561	1103.42	310.4	98%	483.63	109.78
24228	1037.63	336.37	98%	510.12	105.18
5616	1252.37	399.53	98%	617.19	131.84
15189	2393.48	562.64	98%	642.89	398.85
563	1286.12	293.65	98%	647.49	154.22
19392	1380.71	448.01	98%	669.42	123.39
21740	2258.4	588.09	98%	701.14	280.06
1854	2250.76	618.07	99%	730.54	265.59
3292	2871.21	931.15	99%	892.15	311.65
22598	2831.24	966.7	98%	1051.05	357.55
21661	2797.22	982.49	98%	1087.36	376.19
21660	4837.56	1684.22	98%	1692.71	582.02
17167	4555.27	1157.69	98%	2481.92	715.65

TABLE 3N: Early Diclofenac				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non-Group Mean	Non Group Stdev
10667	411.83	248.79	97%	13.74	165.12
17695	47.26	305.83	96%	15.36	60.09
3452	91.31	23.32	97%	29.73	28.67
21421	5.58	8.51	95%	31.49	16.56
6222	-12.72	9.64	95%	32.02	30.46
14996	180.85	117.09	98%	32.69	45.29
12844	-11.84	8.74	96%	39.54	27.67
1843	88.96	20.57	96%	48.67	17.77
9635	-9.83	19.06	95%	48.68	40.62
21707	169.82	64.58	95%	59.13	53.37
23302	37.52	28.79	96%	62.8	26.58
13932	-63.25	79.49	95%	63.9	55.2
18604	24.17	7.4	97%	65.08	25.49
20354	220.66	86.86	98%	66.15	50.9
1841	188.63	53.81	95%	69.83	46.13
355	149.37	52.24	97%	71.24	34.86
17683	40.01	12.49	96%	77.75	25.92
2359	17.87	8.17	98%	86.55	44.73
3713	168.44	419.14	97%	89.98	96.34
11840	51.82	10.03	96%	100.7	37.97
19211	88.71	85.04	96%	108.71	56.23
17800	70.19	39.86	98%	118.7	28.58
1844	277.5	69.37	96%	129.25	44.39
356	249.59	82.38	98%	129.82	46.84
23494	49.03	10.06	96%	131.42	50.45
14776	49.01	22.62	97%	134.61	47.31
23626	251.41	69.01	97%	141.32	90.59
23491	85.95	100.32	96%	155.17	56.53
21382	60.1	10.48	95%	162.86	70.74
6213	75.91	24.03	97%	177.43	53.8
15170	66.01	17.61	95%	180.78	58.76
23182	47.61	14.34	95%	182.97	82.24
14958	77.51	24.88	99%	192.52	57.74
16562	315.91	84.36	96%	194	49.14
23043	116.23	50.3	97%	200.45	58.35
18996	115.11	26.79	96%	211.48	69.45
14997	807.1	529.54	98%	231.67	129.71
10879	84.17	41	95%	235.09	83.29
11021	90.03	69.2	95%	247.67	106.37
2655	43.2	16.5	97%	258.1	178.54
16859	704.09	252.4	97%	258.84	124.37
17794	130.88	63.44	97%	261.13	86.21
6919	1235.49	468.87	99%	269.17	229.63
13353	151.45	114.9	97%	276.39	67.85

TABLE 3N: Early Diclofenac				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
20	432.75	81.44	97%	277.59	75.26
12964	106.32	33.26	95%	288.44	95.46
3722	585.01	101.14	97%	295.66	101.48
20715	308.31	50.21	96%	313.11	180.79
23606	668.08	172.75	97%	313.49	105.76
23230	176.98	99.78	98%	342.52	164.69
12946	142.18	31.13	97%	349.51	100.28
24200	1265.26	395.08	97%	369.8	208.75
16768	264.62	55.65	95%	376.13	78.38
12857	231.61	293.1	96%	392.81	143.31
18795	726.51	149.33	97%	395.27	107.88
19	654.92	135.45	97%	397.11	105.29
18783	716.54	157.61	95%	402.03	119.63
19252	288.39	79.84	95%	410.59	104.1
1114	645.09	101.99	96%	427.86	137.39
20698	914.65	381.61	97%	479.92	178.44
21098	1119.71	394.89	99%	521.35	157.69
21097	883.9	345.03	98%	525.66	142.61
15191	1868.16	232.88	99%	528.3	355.46
19373	957.63	171.61	96%	529.59	254.13
9424	1020	141.63	96%	537.58	150.22
15606	331.04	100.93	95%	555.14	142.5
4670	2609.57	936.24	97%	576.03	466.99
402	1115.89	448.86	99%	596.85	131.13
13557	267.85	27.9	96%	601.37	178.89
2368	429.73	38.72	96%	606.25	88.63
22906	2134.54	974.52	97%	617.58	470.92
15189	1986.69	445.74	98%	635.58	391.8
15190	2159.12	392.22	99%	661.42	378.72
1995	1259.5	439.49	98%	684.23	244.32
11830	1983.61	566.45	98%	692.89	304.27
1805	1229.6	164.21	97%	703.35	218.45
1174	1340.59	440.4	96%	726.33	411.01
6013	1139.77	436.67	96%	749.39	184.56
17785	1846.83	672.05	97%	752.99	445.33
22840	1352.3	529.97	95%	755.78	273.45
8515	346.51	83	96%	765.99	292.49
21574	391.95	100	97%	817.75	226.02
6477	1367.6	542.86	97%	857.33	304.69
3292	1879.44	784.97	98%	890.76	323.1
12306	3293.83	1170.7	99%	1005.26	433.69
7451	1583.77	483.79	96%	1014.48	337.6
6295	2775.87	1040.34	99%	1068.45	493.12
21467	2391.61	1040.88	96%	1118.01	516.67

TABLE 3N: Early Diclofenac				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
6633	2355.01	832.32	99%	1206.88	312.71
14738	2426.79	883.37	99%	1231.22	312.92
3730	2978.69	1180.6	98%	1232.87	586.1
3617	2869.63	1011.46	98%	1268.73	398.2
8715	3069.61	1101.03	99%	1353.63	759.44
17672	2889.9	351.84	96%	1930.21	397.38
26152	5392.56	2027.73	98%	1991.62	852.89
20846	4030.03	570.84	96%	2449.47	889.44
6018	11859.37	4320.03	98%	3477.55	3126.6

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TABLE 30: Estradiol				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
19476	221.25	108.8	94%	-58.59	73.88
20579	65.59	26.23	87%	-13.8	30.61
4520	74.3	35.09	90%	-1.56	34.15
55	34.69	14.89	86%	4.7	13.41
384	44.98	13.2	86%	5.76	28.49
22722	566.51	262.91	96%	19.66	47.88
12120	291.19	164.4	93%	20.32	48.27
16283	59.56	11.97	91%	25.04	15.43
10611	78.35	19.48	91%	26.01	28.58
3570	1203.99	486.89	96%	27.26	139.67
3929	66.1	15.81	88%	32.04	17.87
16783	94.16	35.66	86%	32.29	33.01
6604	9.87	7.84	88%	36.24	17.57
10540	70.62	15.26	85%	39.69	19.11
3846	63.36	11.22	85%	40.64	15.95
14266	463.56	161.4	95%	42	79.9
15097	-4.06	20.79	88%	44.39	28.23
16809	77.26	7.57	89%	53.84	28.46
672	185.2	45.2	92%	57.01	48.59
25290	322.26	83.7	94%	68.08	67.25
5493	104.13	22.09	86%	69.51	45.42
17699	379.25	121.82	95%	77.01	64.08
15057	178.76	62.35	89%	80.64	61.88
4082	137.71	29.22	87%	81.24	39.54
3074	305.3	91.43	94%	82.44	74.5
12655	222.74	65.14	88%	90.1	61.41
3073	404.03	113.1	94%	97.56	106.47
23220	158.44	34.05	86%	104.71	23.6
18612	214.55	48.01	88%	114.72	54.02
24442	253.1	51.52	95%	119.28	39.27
19258	345.84	102.07	91%	119.63	94.13
6789	266.72	63.61	88%	130.61	57.1
11465	687.63	230.97	94%	136.61	114.55
23491	259.04	44.02	89%	151.54	55.44
3075	515.63	145.3	94%	159.61	267.05
19261	291.37	82.45	86%	163.74	57.85
17393	223.13	34.27	86%	164.98	67.02
23987	254.16	41.43	86%	168.68	53.84
13229	314.84	68.95	90%	184.84	61.96
15295	252.4	28.26	85%	191.1	52.8
23183	91.05	26.84	85%	192.16	88.8
6549	522.38	151.13	89%	204.39	114.46
13092	440.75	124.27	92%	206.68	86.61
9402	278.52	27.55	85%	207.63	69.5

TABLE 30: Estradiol				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
23362	362.98	58.85	92%	209.03	55.26
729	141.14	32.05	85%	209.19	55.66
13963	572.36	193.21	91%	220.12	112.51
17516	287.34	30.47	85%	223.48	56.14
7927	368.05	56.64	86%	226.41	79.19
14989	306.39	34.48	90%	229.8	59.41
5464	608.63	139.88	93%	235.86	136.35
14997	313.77	45.38	92%	237.05	156.21
23337	388.86	61.57	87%	239.19	87.95
6541	835.22	410.07	90%	240.86	107.93
9621	349.89	41.41	91%	242.89	62.26
18877	1770.96	536.63	95%	251.02	323.54
19825	76.2	82.83	85%	256.34	107.9
291	413.96	84.34	85%	256.37	66.6
17613	349.67	47.08	86%	259.18	106.99
19824	83.21	81.92	87%	260.01	99.57
7684	577.91	188.77	85%	279.08	126.11
2373	634.92	150.17	92%	285.8	133.51
2484	57.67	44.88	86%	289.53	213.13
16684	447.2	65.17	88%	306.67	87.7
6975	700.83	228.78	86%	312.49	161.5
18141	1086.32	372.55	88%	330.82	216.89
25718	464.33	56.04	91%	331.59	76.26
18742	172.88	37.74	87%	352.25	190.08
12361	1014.46	256.68	94%	354.09	232.49
16327	558.02	61.36	88%	369.06	94.06
21164	169.42	47.37	86%	370.17	185.53
24012	2053.62	525.68	94%	382.21	392.09
4674	167.98	66.36	88%	452.2	224.88
6060	310.86	53.86	86%	477.05	121.08
1561	310.14	86.6	90%	491.78	117.97
11227	841.6	140.02	86%	496.07	212.99
19728	229.27	93.53	88%	501.97	174.65
12746	759.81	83.64	93%	520.3	104.48
12585	909.57	150.85	86%	542.79	178.84
23437	271.75	62.16	86%	558.17	246.21
11821	1051.26	228.29	86%	574.09	309.97
24707	407.68	85.92	85%	598.16	183.22
16894	1105.64	177.51	91%	731.2	332.55
11720	397.65	148.44	88%	748.93	265
4440	398.17	156.94	89%	804.73	210.24
7584	2336.91	636.07	91%	819.41	712.46
13093	2287.36	766.73	90%	825.52	505.38
11644	485.11	142.46	86%	838.95	238.55

TABLE 30: Estradiol				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
9475	422.84	219.9	86%	958.81	372.8
24112	1879.78	259.59	90%	1026.22	630.45
16703	714.02	96.32	86%	1057.6	331.01
15534	1418.23	154.26	88%	1104.88	261.78
14738	862.34	156.54	85%	1256.55	349.62
14960	1831.5	294.22	85%	1370.37	509.8
22554	609.46	270.71	86%	1371.14	511.54
6015	707.01	273.93	89%	1539.98	455.17
7497	1136.4	136.44	87%	1691.66	329.88

TABLE 3P: Late Indomethacin				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
21075	56.56	18.08	99%	-101.64	72.06
3626	270.02	126.67	99%	-91.68	41.85
20522	88.79	62.74	99%	-86.26	44.12
18203	28.03	7.89	100%	-59.65	26.67
21682	139.83	65.11	99%	-56.8	31.49
20119	75.13	51.9	99%	-51.89	22.95
945	164.01	44.63	98%	-32.43	36.01
8017	40.5	7.12	99%	-4.91	18.36
22516	427.71	48.74	100%	-3.53	27.61
7858	133.46	131.64	99%	-2.18	10.32
11731	57.13	15.61	99%	-1.13	13.51
2011	88.53	22.86	99%	5.7	10.46
19121	104.23	50.09	99%	16.77	12.76
24826	218.27	46.71	99%	17.2	179.73
23555	133.19	49.37	99%	22.23	20.8
21445	313.48	71.78	99%	22.36	29.24
1777	117.77	21.2	99%	22.67	16.4
16173	249.12	60.67	99%	23.05	21.76
21683	179.43	48.48	99%	24.37	26.58
19503	106.66	42.52	99%	24.54	12.74
19444	479	225.49	99%	26.17	29.3
20651	252.93	78.27	99%	26.84	24.52
11172	108.09	14.64	99%	27.38	25.08
7196	70.2	6.99	99%	27.5	18.37
8864	168.51	38.98	98%	28.16	40.98
25052	413.35	149.76	98%	28.65	72.19
12277	188.8	30.97	99%	28.87	27.27
20134	115.79	25.97	99%	31.07	21.72
15961	155.48	44.33	99%	31.59	27.65
22897	135.13	41.74	99%	33.43	19.08
1893	250.46	53.73	99%	40.37	21.42
22512	493.75	186.61	99%	40.54	35.84
14081	1307.16	578.37	99%	40.73	109.27
25083	96.77	17.16	99%	41.1	19.54
17500	182.9	29.18	100%	43.12	42.04
2013	191.84	31.9	99%	44.55	23.34
8273	410.92	194.88	99%	45.89	30.96
19411	184.69	32.53	99%	46.1	23.55
15504	896.04	321.22	99%	46.28	53.42
22514	543.21	150.84	99%	57.67	44.72
155	187.91	27.8	99%	62.07	21.49
20523	337.44	89.8	98%	66.71	58.22
16961	225.29	41.42	99%	71.58	40.53
24589	412.43	149.59	98%	73.14	30.15

TABLE 3P: Late Indomethacin				Document Number 1659775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
21285	903.94	338.62	99%	73.28	108.74
15503	519.54	109.49	100%	74.61	27.28
6200	1572.18	522.18	99%	78	145.78
7743	288.96	85.4	98%	83.77	52.71
2012	357.34	70.02	99%	84.87	34.39
3749	-48.1	12.54	99%	87.36	48.17
4892	2121.77	1018.81	99%	97.96	339.86
24651	168.51	30.23	98%	98.36	20.05
23005	536.62	86.56	99%	99.43	90.49
1700	273.11	39.16	99%	102.11	30.56
22898	507.42	174.82	99%	103.97	57.4
8522	552.47	146.35	99%	105.43	54.02
12714	0.7	18.22	98%	106.47	34.92
15116	243.85	52.64	98%	107.4	25.94
17277	239.1	35.46	99%	107.78	39.78
22042	21.05	10.38	98%	109.25	91.56
21414	1412.18	189.99	99%	116.04	143.33
17258	235.7	32.66	99%	120.39	25.05
682	555.72	137.48	99%	126.28	58.1
17369	441.37	64.2	99%	130.38	54.83
20529	790.13	186.87	99%	134.07	101.45
14504	773.65	116.14	99%	147.38	84.22
154	347.17	63.6	99%	154.37	37.49
12450	-60.33	24.42	99%	154.48	84.94
6431	1828.3	421.64	99%	190.99	149.33
18580	1167.73	411.76	99%	193.7	141.11
8310	107.35	13.86	99%	204.96	44.79
14330	633.28	126.05	99%	225.12	77.1
5687	48.78	22.59	99%	227.66	79.73
14185	760.34	170.85	99%	253.08	93.43
21443	569.4	110.65	99%	256.7	61.78
16519	807.19	191.58	98%	273.02	117.31
9079	820.52	184.52	98%	316.54	112.19
19469	162.04	26.75	99%	325.82	57.22
373	115.43	31.34	99%	334.03	85.91
43	156.53	22.34	99%	341.11	74.71
20864	37.65	12.15	100%	352.3	179.09
699	762.57	112.9	99%	383.6	79.72
24323	230.34	24.71	99%	398.78	95.09
17281	100.34	30.42	99%	410.15	105.21
16366	113.72	34.12	99%	439.22	103.99
21014	188.22	42.97	99%	572.37	137.02
16367	166.59	86.34	99%	612.27	144.06
25525	264.07	72.58	99%	645.12	117.62

TABLE 3P: Late Indomethacin				Document Number 1550775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
635	308.38	68.87	99%	672.17	126.74
18890	126.36	42.96	99%	679.93	361.87
634	355.69	72.95	99%	705.77	125.16
6236	227.28	73.91	98%	902.24	429.28
10984	135.85	78.66	99%	1092.48	362.92
15029	181.72	50.19	99%	1492.95	529.6
4933	357.28	114.44	99%	1702.56	598.89

TABLE 3Q: Early Indomethacin				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non_Group Mean	Non_Group Stdev
21682	85.12	87.03	93%	-56.37	33.66
1510	75.53	7.54	96%	-13.1	65.66
26280	109.21	31.74	89%	-10.05	85.78
11422	60.74	22.85	91%	13.75	11.38
1507	46.96	9.51	87%	15.4	15.74
16251	34.42	5.87	90%	20.02	13.62
19671	39.81	7.46	90%	22.33	14.64
23106	48.6	11.99	93%	28.28	33.85
2736	49.82	5.14	93%	29.89	18.47
25077	111.99	30.35	88%	30.69	73.6
1221	445.47	178.19	92%	33.57	94.3
18389	94.31	16.02	94%	33.62	32.95
3972	-24.58	15.09	94%	34.18	35.89
18237	63.23	7.16	91%	36.35	20.91
22725	4.84	8.57	88%	36.54	24.3
17854	94.21	22.12	90%	48.6	21.13
25379	64.97	7.1	91%	48.71	16.47
1843	85.73	19.01	94%	48.71	17.88
4504	96.84	28.13	90%	48.77	77.49
24024	75.74	15.08	90%	50.05	33.85
16809	117.87	32.17	90%	53.62	27.39
11423	102.73	23.05	89%	54.5	20.13
2042	92.88	5.97	96%	54.98	50.98
13992	110.02	45.53	90%	55.81	24.86
22918	27.24	5.2	92%	57.51	29.32
5059	222.71	98.2	92%	61.9	61.99
20354	194.32	79.46	91%	66.49	51.97
18529	139.38	36.52	88%	68.68	53.21
8079	-1.13	28.24	91%	70.82	43.57
7176	83.8	6.04	89%	71.68	21.23
24721	116.01	17.12	91%	75.35	29.71
11904	169.62	30.75	91%	81.73	37.23
3710	-40.52	24.79	89%	84.89	112.56
1271	127.09	19.36	88%	87.87	22.54
15207	207.84	67.65	90%	88.03	53.57
21256	150.53	29.3	87%	90.66	43.12
1572	134.45	17.05	87%	92.3	26.58
19410	154.21	25.11	89%	95.44	23.68
16080	172.16	50.03	89%	95.77	117.15
17950	134.99	16.51	87%	96.23	39.64
22321	169.07	47.34	95%	101.03	89.08
9223	166.07	27.83	88%	106.75	43.32
17277	186.86	45.28	88%	108.27	41.12
16125	212.34	60.78	90%	109.55	34.54

TABLE 3Q: Early Indomethacin				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
354	156.92	39.75	88%	113.78	121.78
22151	49.94	21.66	90%	114.35	59.07
16477	205.91	47.02	87%	118.16	42.37
15884	197.78	19.66	96%	119.51	58.67
25768	189	17.68	94%	128.02	30.12
6532	275.04	58.08	92%	135.65	42.31
2555	342.38	116.88	91%	141.73	57.69
25370	95.55	12.34	87%	141.81	76.1
1426	186.05	11.71	91%	141.89	28.02
16081	293.29	79.31	90%	147.43	146.68
154	240.39	32.25	90%	155.47	42.04
1521	271.17	53.27	87%	157.16	61.75
22806	82.54	19.97	89%	169.69	77.1
1141	221.49	23.61	89%	172.77	35.13
9595	369.54	72.63	90%	176.26	67.68
21709	240.64	11.92	95%	179.9	33.86
13332	111.82	16.97	88%	187.21	61.88
21444	292.61	40.73	91%	204.56	58.9
20350	333.21	45.66	91%	216.95	69.67
3776	316.54	58.6	88%	226.04	54.29
958	283.88	16	89%	240.09	72.64
18891	63.95	40.8	91%	245.89	190.12
15786	130.41	48.25	89%	247.11	88.8
22619	509.69	128.09	87%	254.11	122.09
2655	76.89	36.89	90%	257.67	178.99
21443	408.93	75.59	90%	258.32	68.58
17664	718.76	159.35	90%	309.86	189.82
1795	179.95	54.13	87%	340.51	149.15
6825	188.01	57.66	89%	342.19	121.17
18465	583.12	68.3	93%	353.78	236.17
19412	798.48	156.59	91%	364.41	124.75
4026	854.17	324.83	92%	368.96	133.71
20915	208.25	51.68	88%	381.94	139.96
12463	631.37	114.76	89%	391.56	105.49
7122	778.65	154.65	89%	421.1	129.61
23245	695.04	100.61	88%	453.5	126.98
20701	818.5	138.91	89%	496.14	169.1
23125	203.3	56.02	88%	520.99	516.04
21740	1357.78	289.81	91%	701.6	296.47
16458	933.78	80.79	89%	722.78	196.14
11720	1393.76	333.85	92%	731.5	257.06
23449	166.05	104.49	89%	922.94	660.67
23989	1702.06	285.92	87%	1063.27	404.32
22368	637.02	202.48	88%	1081.65	343.44

TABLE 3Q: Early Indomethacin				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
24289	672.7	120.08	88%	1097.27	342.03
16885	837.41	195.77	91%	1485.4	407.68
9267	809.11	323.93	92%	1667.39	543.29

TABLE 3R: Valproate				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
26190	239.04	44.21	99%	-115.53	71.46
2154	26.52	22.45	98%	-34	15.98
12625	129.76	35.25	98%	-7.97	79.74
4231	160.07	13.84	100%	-6.47	34.51
360	42.77	15.77	97%	-5.58	16.63
24126	127.21	24.22	97%	6.68	31.59
8993	64.31	7.77	99%	8.92	10.71
19762	168.43	71.93	99%	9.69	24.52
11336	60.09	15.29	99%	12.42	10.72
20993	73.86	17.79	98%	12.51	23.49
330	76.9	11.84	98%	13.5	26.03
12058	48.89	5.96	98%	16.85	15.53
1579	75.5	19.78	98%	16.86	13.09
5993	49.43	5.91	97%	17.56	13.02
8054	63.83	11.7	97%	17.56	15.18
23315	53.08	6.14	98%	20.16	11.05
23843	102.85	21.92	99%	21.2	18.22
11315	170.88	30.14	98%	22.9	42.27
13812	138.26	33.46	99%	26.62	22.64
23106	97.66	12.04	99%	28.05	33.33
11625	70.95	9.83	97%	28.43	16.22
9374	155.52	11.78	99%	30.44	41.52
10394	210.39	57.19	99%	35.12	29.91
6101	146.33	49.53	97%	38.17	25.87
2117	107.64	17.82	97%	43.75	19.24
12614	113.54	14.75	98%	45.51	37.01
9766	130.53	51.66	98%	47.22	33.17
2932	256.87	86.84	98%	48.26	30.66
13501	145.64	35.69	98%	48.87	22.87
14913	145.2	21.59	98%	51.42	27.75
16673	133.08	23.07	98%	53.6	21.07
2042	183.57	50.07	98%	54.55	49.7
2915	150.2	35.95	98%	55.29	23.13
19669	192.83	28.28	99%	60.25	31.79
19264	145.96	13.12	98%	62.26	25.95
17257	197.58	17.21	99%	67.22	34.6
15663	157.22	12.55	98%	67.92	42.04
11527	186.56	12.56	97%	68.89	53.83
22375	201.22	32.17	99%	75.66	28.1
5754	289.15	110.18	98%	82.52	54.48
12198	157.09	5.38	99%	83.53	37.27
18885	179.92	14.06	99%	85.54	27.13
13166	392.55	98.9	98%	89.27	56.47
13251	155.07	11.85	97%	89.73	88.96

TABLE 3R: Valproate				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
8728	346.01	114.17	98%	90.12	40.25
2216	234.47	28.59	99%	94.87	37.16
21535	197.23	12.53	98%	96.15	38.42
21567	509.19	66.46	98%	97.9	104.57
10593	328.02	63.73	99%	101.91	43.97
17368	241.72	37.58	97%	104.44	49.02
9800	366.46	11.6	99%	105.66	68.67
17479	261.87	40.08	99%	106.14	33.44
21976	256.5	24.3	98%	106.4	45.51
14600	242.39	40.76	98%	111.36	76.44
22570	241.74	26.13	97%	111.56	44.08
23656	273.7	31.03	98%	112.56	52.23
15179	255.98	37.97	98%	112.9	41.1
16616	304.19	58.02	98%	115.37	49.86
5608	233.3	11.25	97%	122.33	53.28
20090	263.76	45.31	98%	126.59	32.66
17644	333.21	52.99	98%	128.35	68.07
15149	345.13	64.29	97%	128.59	59.92
6789	283.91	53.49	99%	133.02	59.87
6686	369.2	41.65	99%	139.06	46.36
19230	391.37	57.35	98%	149.61	84.83
13949	47.22	6.84	99%	151.24	58.29
11280	287.5	36.75	98%	159.37	38.65
19513	345.16	59.75	97%	163.49	60.93
23762	321.28	26.82	97%	164.97	66.22
13838	437.29	30.14	99%	166.7	55.87
2691	316.24	12.09	98%	168.14	70.13
9572	409.53	66.85	99%	168.33	60.29
6861	397.87	34.78	100%	168.71	47.4
22135	361.16	95.89	98%	170.63	47.21
24388	283.3	44.23	98%	172.33	155.38
18886	403.05	74.14	98%	175.49	63.14
24368	602.67	63.22	99%	183.22	79.82
5381	356.13	13.85	99%	191.57	49.01
9402	342.47	21.74	97%	208.49	68.96
17261	546.81	71.98	99%	219.95	72.35
2101	430.5	35.07	99%	224.81	67.09
24369	546.78	56.44	97%	228.98	103.39
11354	530	66.53	99%	229.49	68.24
8709	90.79	24.72	98%	233.09	61.98
24367	400.74	12.79	99%	245.59	55.58
19052	646.73	83.13	98%	254.53	92.68
22957	665.35	87.82	98%	274.44	208.86
15551	493.87	26.61	99%	304.36	63.07

TABLE 3R: Valproate				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
12317	639.88	73.89	99%	308.65	88.02
4179	845.91	78.29	98%	333.97	135.14
6440	961.78	166.32	97%	351.53	186.44
7111	553.56	43.59	98%	353.19	75.73
18285	707.67	76.76	99%	357.46	132.75
12928	791.23	86.89	98%	410.91	94.08
15051	1110.61	136.73	97%	476.75	412.42
2569	338.95	14.84	98%	721.15	290.78
3803	499.92	74.41	97%	920.04	208.7
18962	573.38	98.13	99%	1606.33	624.84
5052	906.23	65.55	99%	1930.67	442.76
22540	1108.89	178.44	97%	2311.11	657.83

TABLE 35: WY-14643 Document Number 1650775

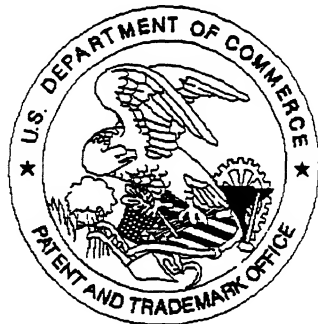
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
3175	81.67	38.5	98%	-24.57	20
2051	31.61	16.91	98%	-19.67	25.77
23627	40.97	4.93	98%	-14.82	37.36
16409	95.86	23.34	97%	-8.25	35.38
14116	38.83	17.55	99%	-7.83	5.25
18029	208.84	94.33	98%	-7.23	21.53
6677	32.1	15.65	98%	-6.62	9.95
20856	275.88	94.5	99%	-5.26	14.41
5565	221.64	85.1	97%	17.46	47.37
12467	216.39	65.04	99%	20.32	20.78
23500	148.59	59.24	99%	22.05	17.54
1858	529	114.56	99%	23.94	68.23
8820	81.06	9.86	99%	28.61	31.53
18082	128.62	31.47	99%	29.7	16.97
4931	135.4	29.63	97%	33.8	32.95
9925	117.26	29.18	98%	42.43	17
24381	97.68	12.7	98%	43.65	17.97
6292	96.5	10.27	98%	43.76	16.97
5518	-34.55	15.68	100%	44.56	14.44
18083	370.91	74.26	98%	45.23	60.06
4272	590.58	82.76	100%	47.77	61.51
7295	114.22	11.36	98%	48.54	27.07
8315	251.82	52.39	98%	50.52	44.35
20855	205.89	56.89	100%	51.41	13.97
15018	153.93	12.99	97%	51.69	40.82
22046	173.79	36.81	97%	52.05	35.05
4438	-53.05	31.71	99%	53.83	12.81
18956	233.24	49.47	99%	57.47	28.38
3631	135.16	24.43	97%	62.18	23.06
4271	1146.85	102.6	100%	63.33	94.28
6553	215.81	43.91	97%	64.81	42.7
3558	192.81	32.74	98%	65.12	31.67
20038	306.38	66.25	98%	68.41	50.76
7517	190.58	26.66	98%	71.67	32.59
3743	185.35	31.74	99%	71.95	25.24
14507	291.71	54.52	98%	74.57	66.85
18749	288.03	90.54	98%	77.94	40.13
4290	293.68	45.21	98%	87.32	46.32
14595	321.16	55.3	98%	89.33	56.57
14264	331.35	82.51	98%	91.8	58.3
397	232.66	39.79	99%	91.99	32.22
18746	280.52	43.35	98%	93.45	48.78
3439	244.57	26.7	99%	100.37	28.67
2190	164.79	17.03	97%	100.78	189.02

TABLE 3S: WY-14643				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
18318	279.93	40.82	98%	111.57	48.48
5887	1076.32	275.73	99%	111.64	138.98
3513	212.58	33.36	98%	114.18	27.84
22416	1001.99	170.33	99%	121.52	83.97
22224	487.47	76.85	99%	124.54	72.09
12215	632.99	209.38	98%	141.79	100.45
9373	419.3	49.02	98%	144.86	76.23
15672	378.23	65.03	98%	151.17	68.05
3260	508.28	175.97	98%	153.29	72.65
16700	596.39	103.44	99%	155.05	96.4
18747	457.04	82.08	97%	155.98	76.29
26109	1286.05	121.59	99%	156.58	201.4
22737	685.5	206.71	99%	168.28	96.83
3720	315.08	30.72	98%	179.69	49.62
2113	410.43	34.36	99%	185.32	58.03
15015	374.26	31.51	99%	192.11	63.36
6439	425.56	74.96	97%	196.56	74.01
22370	945.85	62.98	100%	216.15	108.38
2457	1132.75	158.6	99%	227.31	140.2
1728	477.23	66.78	98%	227.92	60.65
18891	1245.42	225.38	99%	230.61	151.12
22620	386.56	21.42	98%	235.22	68.77
19591	567.11	40.94	99%	237.04	108.52
5602	1404.36	215.76	99%	242.82	212.8
24860	67.15	34.2	97%	279.45	115.83
22392	598.76	55.66	99%	296.04	67.51
18742	1303.27	263.5	99%	335.32	154.05
6825	626.39	47.06	98%	336.52	118
21164	991.37	155.11	99%	356.95	172.12
9372	1244.96	107.3	99%	368.29	225.64
8177	121.78	23.64	97%	389.45	423.88
17935	1404.15	220.52	97%	416.54	273.3
10533	1054.36	147.32	98%	421.36	212.4
16944	747.42	72.2	98%	422.41	133.98
21354	2186.83	317.02	98%	437.51	348.77
16323	223.57	44.79	99%	465.4	220.36
9423	273.32	30.42	98%	486.76	134.12
19044	814.58	45.86	97%	502.31	184.58
18727	206.23	25.52	99%	516.82	179.53
18125	1062.51	80.83	99%	529.14	174.32
16704	1486.63	221.63	97%	565.52	242.61
3099	922.46	83.44	97%	599.33	119.33
2813	1250.39	172.69	98%	603.02	185.25
20998	325.2	72.5	97%	606.04	134.27

TABLE 3S: WY-14643				Document Number 1650775	
GLGC ID	Group Mean	Group Stdev	LDA Score	Non Group Mean	Non Group Stdev
21010	1699.76	218.74	98%	606.25	249.41
14882	377.63	34.39	97%	607.89	168.14
5616	386.99	47.15	97%	623.82	140.57
16945	1098.96	98.19	98%	628.67	192.67
7420	1415.94	79.85	97%	655.69	311.93
18890	1900.82	258.12	99%	657.78	337.82
3279	1571.19	374.24	98%	708.13	199.08
16190	1581.05	206.33	98%	716.2	226.42
20597	378.94	48.6	98%	742.21	189.37
21341	1797.23	203.99	98%	768.53	328.94
4940	623.22	140.4	98%	1632.44	469.8

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